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DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00534; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PS00722; CHYMOTRYPSIN.
DR PRINTS; PS00722; CHYMOTRYPSIN.
DR PRINTS; PS00001; GLABLOOD.
DR PRINTS; PS00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00022; EGF_2; UNKNOWN_1.
DR PROSITE; PS01186; EGF_CA; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 100.0%; Score 46; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 371 LVDRATCLR 379

RESULT 2
ID Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7; 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_TaxID=5986;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
chimpanzees.";
RL Genes Genet. Syst. 0.0-0(2001).
DR EMBL; AB062471; BAB58886.1; JOINED.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; ASX_Hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000842; EGF_2.
DR InterPro; IPR001254; Ser-protease Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00534; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00022; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF6585 CRC64;

Query Match 100.0%; Score 46; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 376 LVDRATCLR 384

RESULT 4
ID Q96516 PRELIMINARY; PRT; 908 AA.

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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR KW Hydrolase; Serine protease.
DR SQ SEQUENCE 461 AA; 51764 MW; 30C2F957C0F77F45 CRC64;

Query Match 100.0%; Score 45; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 376 LVDRATCLR 384

RESULT 3
ID Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6; 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_TaxID=5986;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=505;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
chimpanzees.";
RL Genes Genet. Syst. 0.0-0(2001).
DR EMBL; AB062471; BAB58886.1; JOINED.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; ASX_Hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000842; EGF_2.
DR InterPro; IPR001254; Ser-protease Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00534; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00022; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase; Serine protease.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF6585 CRC64;

Query Match 100.0%; Score 46; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 376 LVDRATCLR 384

RESULT 4
ID Q96516 PRELIMINARY; PRT; 908 AA.

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RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL NZ;
RA      Waterston R.;
RR      *Direct Submission.";
RRL      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RRL      EMBL; AF077541; AAC64633.1; -.
DR      InterPro; IPR002308; Cys_rRNA-synt_1a.
DR      InterPro; IPR002308; Cys_rRNA-synt_1a.
DR      PRINTS; PR00943; TRANSANTHCVS.
DR      TIGRFAM; TIGR00435; cybS; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 909 AA; 105316 MW; FDFAE96133864DAC CRC64;

Query Match      78.3%; Score 36; DB 5; Length 909;
Basic Local Similarity 78.3%; Prev. N 73.0%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  LVDRAATCLR 9
DB      811 LVDRAATCLR 819
      |||||
      |||||

RESULT 6
QVALS      PRELIMINARY; PRT; 60 AA.
ID  Q9U4L5
AC  Q9U4L5;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DR      Mitotic cyclin-like protein (fragment).
KW      Cyclin
KW      T.
KW      Tetrahymena thermophila
KW      Tetrahymena; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
KW      Eukaryota; Alveolata; Tetrahymena.
KW      NCBI TaxID=5911;
EN  [1]
RN  [1]
RC      SEQUENCE FROM N.A.
RR      STRAIN=CU427; Ong X., Berger J.D.;
RR      *Yang L.H., like sequence in Tetrahymena thermophila.";
RRL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RRL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC  CC  -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR      EMBL; AF165220; AFI5554.1; -.
DR      HSSP; P30774; 1VIN.
DR      InterPro; IPR004366; Cyclin.
DR      InterPro; IPR004366; Cyclin.
DR      SMART; SM0038; Cyclin; 1.
DR      SMART; SM0038; Cyclin; 1.
DR      PROSITE; PS00292; CYCLINS; 1.
KW      Cell cycle; Cell division; Cyclin.
KW      NON_TER 1
KW      NON_TER 1
SQ      SEQUENCE 60 AA; 7020 MW; 803EC056F3D45D2 CRC64;

Query Match      73.9%; Score 34; DB 5; Length 60;
Basic Local Similarity 73.9%; Prev. N 70.4%;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  LVDRAATCLR 9
DB      34 LVDRAATCTR 41
      |||||
      |||||

RESULT 7
QVALS      PRELIMINARY; PRT; 254 AA.
ID  Q01136
AC  Q01136;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DR      Trypsin-like protease 1 precursor.
KW      Trypsin-like protease 1 precursor.
KW      Metaphizium anisopliae
KW      Buxarjofa; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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OC Hypocitales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.  
 RN NCBI\_TaxID=5530;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RA Smithson S.L., Peterson S.L., Bailey A.M., Screen S.E., Hunt B.A.,  
 RA Cobb B.D., Cooper R.M., Charnley A.K., Clarkson J.M.,  
 RA "Cloning and characterisation of a gene encoding a cuticle-degrading  
 protease from the insect pathogenic fungus Metarhizium anisopliae.",  
 RL Gene 166:161-165 (1995).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 AC HYDROLASE; Serine protease; Signal.  
 CC EMBL: X78875; CAA55477.1; --  
 DR HSSP: P35049; ITRY.  
 DR MEROPS: S01.103; --  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser. protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase: Protease; Serine protease; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 SQ SEQUENCE 254 AA; 26117 MW; 0ABD96A5C53DBA34 CRC64;  
 Query Match 73.9%; Score 34; DB 3; Length 254;  
 Best Local Similarity 85.7%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATC 7  
 DB 169 VDRATC 175  
 RESULT 8  
 QY7A9 PRELIMINARY; PRT; 255 AA.  
 AC Q9Y7A9  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 GN Trypsin-related protease.  
 OS Metarhizium anisopliae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocitales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.  
 RN NCBI\_TaxID=5530;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RA Screen S.E., St Leger R.J.;  
 RA "Isolation of multiple protease genes from the entomopathogenic fungus  
 Metarhizium anisopliae.",  
 RL Submitted (FEF-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 AC HYDROLASE; Serine protease; Signal.  
 CC EMBL: X78875; CAA55477.1; --  
 DR HSSP: P00763; IDPO.  
 DR MEROPS: S01.103; --  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser. protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase: Protease; Serine protease; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 SQ SEQUENCE 255 AA; 26289 MW; 88DD979ED300E4B7 CRC64;  
 Query Match 73.9%; Score 34; DB 3; Length 255;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATC 7  
 DB 171 VDRATC 177  
 RESULT 10  
 QYK17 PRELIMINARY; PRT; 434 AA.  
 AC QYK17  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 GN Citrate synthase.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 RN NCBI\_TaxID=176299;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RA MEDLINE=21608550; PubMed=11743193;  
 RX MEDLINE=21608550; PubMed=11743193;

Query Match 73.9%; Score 34; DB 3; Length 255;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATC 7  
 DB 173 VDRATC 179  
 RESULT 9  
 QY842 PRELIMINARY; PRT; 256 AA.  
 AC QY842  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 GN Trypsin-related protease precursor.  
 OS Metarhizium anisopliae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocitales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.  
 RN NCBI\_TaxID=5530;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RA Screen S.E., St Leger R.J.;  
 RA "Isolation of multiple protease genes from the entomopathogenic fungus  
 Metarhizium anisopliae.",  
 RL Submitted (FEF-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 AC HYDROLASE; Serine protease; Signal.  
 CC EMBL: AJ242736; CAB44652.1; --  
 DR HSSP: P35049; ITRY.  
 DR MEROPS: S01.103; --  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser. protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase: Protease; Serine protease; Signal.  
 FT SIGNAL 30 256  
 SQ SEQUENCE 256 AA; 26201 MW; 34656608745CB982 CRC64;  
 Query Match 73.9%; Score 34; DB 3; Length 256;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATC 7  
 DB 171 VDRATC 177  
 RESULT 10  
 QYK17 PRELIMINARY; PRT; 434 AA.  
 AC QYK17  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 GN Citrate synthase.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 RN NCBI\_TaxID=176299;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RA MEDLINE=21608550; PubMed=11743193;  
 RX MEDLINE=21608550; PubMed=11743193;



RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Kaur V., Zhou Y., Chen L., Wood G.E., Almeida M.F. Jr., Moo L.,  
 RA Cui Y., Paulsen O., Olsen M.V., Olsen M.V., Olsen M.V.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kuyavin T., Levy R., Li M.-J., McGlelland S., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krepan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Oster R.M., Olsen M.V., Olsen M.V., Olsen M.V., Olsen M.V.,  
 RT C58, "Genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT Science 294:2317-2323 (2001).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Wallin L.,  
 RA Hummel K., Gordon S., Vaudaux K., Adenazi N., Halling C.,  
 RA Wollan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursan J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.,  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58";  
 RL Science 294:2323-2328 (2001).  
 RW EMBL; AB007196; AKS0682.1; ALT\_INIT.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 434 AA; 48002 MW; C5FDBDPA56B01E28 CRC64;

Query Match 73.9%; Score 34; DB 16; Length 434;  
 Best Local Similarity 66.7%; Pred. No. 54;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVDRATCLR 9  
 Db 14 LIQRETCCLR 22

RESULT 11  
 ID Q45148 PRELIMINARY; PRT; 70 AA.  
 AC Q45148;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF11609.  
 OS Bacteroides fragilis.  
 OC Bacteria; CF8 group; Bacteroidetes; Bacteroidales; Bacteroidaceae;  
 OC Bacteroides fragilis.  
 OK NCBI\_Taxid=817;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95291442; PubMed=7773395;  
 RA Trinh S., Haggoud A., Reyssat G., Sebald M.;  
 RT "Plasmids p1941 and p19421 from Bacteroides 5-nitroimidazole  
 RT resistance genes 507 and 5081 upstream insertion elements";  
 RL J Biol Chem 272:11233-11235 (1997).  
 DR EMBL; X76949; CAA54271.1.  
 SQ SEQUENCE 70 AA; 8173 MW; 2C8A7955JA919FF3 CRC64;

Query Match 71.7%; Score 33; DB 2; Length 70;  
 Best Local Similarity 62.5%; Pred. No. 14;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVDRATCLR 8  
 Db 57 MLDKATCLR 64

RESULT 12  
 ID Q516M6 PRELIMINARY; PRT; 165 AA.

AC Q516M6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Hypothetical protein PA0261.  
 GN PA0261.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OK NCBI\_Taxid=287;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437137; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,  
 RA Hickey M.J., Brinkman P.S.L., Huynh W.O., Kowalik D.J., Lagrou M.,  
 RA Garbaye R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Goltzy S.N., Volger K.K., Adair K., Jarbig K., Kim R.M.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen";  
 RT Nature 406:959-964 (2000).  
 RW EMBL; AB004464; AAG03650.1; -.  
 DR Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 165 AA; 18391 MW; C3ED1A0R251C7B CRC64;

Query Match 71.7%; Score 33; DB 16; Length 165;  
 Best Local Similarity 75.0%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVDRATCLR 8  
 Db 145 MLDKATCLR 152

RESULT 13  
 ID Q8W599 PRELIMINARY; PRT; 212 AA.  
 AC Q8W599;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 24, Last sequence update)  
 DE CBP-like protein.  
 OS Secale cereale (Rye).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC SpERMophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Secale.  
 OK NCBI\_Taxid=4550;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21563065; PubMed=11706173;  
 RA Jaglo K.R., Kleff S., Amundsen K.L., Zhang X., Haake V., Zhang J.Z.,  
 RA Deltis T., Thomashow M.F.;  
 RT "Components of the Arabidopsis C-Repeat/Dehydration-Responsive Element  
 RT Binding Factor Cold-Response Pathway Are Conserved in Brassica napus  
 RT and Other Plant Species";  
 RL Plant Physiol 130:1017-1025 (2001).  
 DR EMBL; AF170728; AAL35759.1.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2-domain; 1.  
 DR ProDom; PD001423; TF\_AP2; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 212 AA; 23291 MW; E1D0265030102159 CRC64;

Query Match 71.7%; Score 33; DB 10; Length 212;  
 Best Local Similarity 75.0%; Pred. No. 43;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVDRATCLR 8  
 Db 86 MLDKATCLR 93

RESULTS	14
QW236	
ID	PRELIMINARY; PRT; 212 AA.
IC	QW236;
AD	01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TRENBLrel. 20, Last annotation update)
DD	Purative CRF/DRB-binding factor.
DE	CBF1.
OS	Triticum aestivum (Wheat).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooidae; Gramineae; Triticum.
OC	111_7481d=4385;
RP	SEQUENCE FROM N.A.
RN	STRAIN=CV. WINOKA;
RC	MEDLINE=21563065; PubMed=11706173;
RA	Jaglo K.R., Kleef S., Amundsen K.L., Zhang X., Zhang J.Z., Pelle T., Tomshaw M.; Popsis C.-Repeat/Dehydration-Responsive Element Binding Factor Cold-Response Pathway Are Conserved in Brassica napus and Other Plant Species";
RT	Plant Physiol. 127:910-917(2001).
RL	EMBL; AF376136; AAL37944.1.
DR	InterPro; IPROU1471; TF.ERF.
DR	Plan; PF00847; AP2-domain; 1.
DR	SMART; SM00380; AP2_A2; 1.
SO	SEQUENCE 212 AA; 21336 MW; 585C26DDB6EA2BD CRC64:

Query Match	71.7%	Score 33;	DB 10;	Length 212;
Best Local Similarity	75.0%	Pred. No. 43;		
Matches 6;	Conservative	1;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy	1	LVDRATCL	8
		: : : :	
Db	86	LLDRAACL	93

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RESULT 15
QSVB7
ID QSVB7 PRELIMINARY; PRT: 252 AA.
AC QSVB7
AD QSVB7
DT 01-MAR-2002 (TRENMBrel_20, Created)
DT 01-MAR-2002 (TRENMBrel_20, Last sequence update)
DT 01-MAR-2002 (TRENMBrel_20, Last annotation update)
DE Leza repressor-like protein.
OS ORFL6.
GN ORFL6.
GC ORFL6.
CC ORFL6.
OC Terrabacter sp.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococccinae; Intrasporangiaceae; Terrabacter.
NC NC.
NW 111
PI 111
PR STRAIN=DF63;
RC RC.
RP SEQUENCE FROM N.A.
RR RR.
RT RR.
RT Kaseuga X., Nojiri H., Yamane H., Kodama T., Omori T./
RT "Cloning and characterization of genes involved in the degradation of
RT glucosecuran by Terrabacter sp. strain DF63."
RL EMBL: AB044563; BAB78770.1; J991(1997).
RL EMBL: AB044563; BAB78770.1; J991(1997).
DR Inter-Pro: IPR001647; HTH TetR.
DR Inter-Pro: IPR000159; Peptidase_S24.
DR Pfam: PF00717; Peptidase_S24; 1.
DR Pfam: PF00440; tetR1.1.
DR Pfam: PF00440; tetR1.1.
DR PRINTS: PR00726; LEVASEPTASE.
SQ SEQUENCE 252 AA; 27167 MW; B7C5HACE59ADB3A CRC64;

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Query Match 71.7%; Score 33; DB 2; Length 252;  
Best Local Similarity 85.7%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1	46	100.0	271	1	FA9_PIG	PI6293	sus scrofa
2	2	46	100.0	282	1	FA9_SHEEP	PI6591	ovis aries
3	3	46	100.0	274	1	FA9_RAT	PI6296	rattus norv
4	4	46	100.0	285	1	FA9_CANPO	PI6295	cavia porcea
5	5	46	100.0	455	1	FA9_CANER	PI6294	bos taurus
6	6	46	100.0	455	1	FA9_CANER	PI6294	equus caballus
7	7	46	100.0	459	1	FA9_MOUSE	PI6294	mus musculus
8	8	46	100.0	461	1	FA9_HUMAN	PI6294	homo sapien
9	9	42	91.3	576	1	FA9_RABIT	PI6292	oryctolagus
10	10	36	78.3	586	1	VP40_ILTVT	P23984	cyticellus
11	11	34	73.9	2347	1	XROS_HUMAN	P08922	homo sapien
12	12	33	71.7	123	1	UL55_HGKWA	PI6746	homo sapien
13	13	33	71.7	123	1	UL55_HGKWA	PI6746	homo sapien
14	14	33	71.7	123	1	Y232_HUMAN	Q91895	homo sapien
15	15	32	69.6	268	1	GLCR_HUMAN	Q91895	homo sapien
16	16	32	69.6	311	1	MYRB_MICRG	P43433	micromonospora
17	17	32	69.6	323	1	CMGB_BACSU	P25954	bacillus subtilis
18	18	32	69.6	547	1	ICA3_HUMAN	P32942	homo sapien
19	19	32	69.6	688	1	CHLB_CHLRE	P36347	chlamydomonas
20	20	32	69.6	663	1	LDVR_CHICK	P98165	gallus gallus
21	21	32	69.6	704	1	RAAL_HUMAN	Q03001	homo sapien
22	22	32	69.6	704	1	RAAL_HUMAN	Q03001	homo sapien
23	23	31	67.4	378	1	PROB_BRUNE	Q04779	methylobacillus
24	24	31	67.4	378	1	PROB_BRUNE	Q04779	methylobacillus
25	25	31	67.4	431	1	SCG6_RAT	Q64375	rattus norv
26	26	31	67.4	437	1	N055_HUMAN	Q92791	homo sapien
27	27	31	67.4	873	1	LDVR_MOUSE	P98155	homo sapien
28	28	31	67.4	873	1	LDVR_MOUSE	P98155	homo sapien
29	29	31	67.4	873	1	LDVR_RABIT	P35953	oryctolagus
30	30	31	67.4	873	1	LDVR_RABIT	P35953	oryctolagus
31	31	30	65.2	103	1	CHLB_LVCAN	P98166	rattus norv
32	32	30	65.2	103	1	CHLB_LVCAN	P98166	rattus norv
33	33	30	65.2	103	1	CHLB_LVCAN	P37847	lycopodium
34	34	30	65.2	103	1	CHLB_LVCAN	P37847	lycopodium
35	35	30	65.2	212	1	LYAXA_PNECA	Q07972	pneumocystis

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EMBL; X82593; CAA63337.1; .
PDB; 1PEX; 17-AUG-96.
DR DR MEROPS; S01.214; .
DR DR InterPro; IPR001254; Ser protease_Try_
DR DR InterPro; IPR000294; Vlk_dep_GLA_
DR DR Pfam; PF00089; Trypsin; 1
DR DR PROSITE; PS00011; TRYPSIN_DOM; 1
DR DR PROSITE; PS00134; TRYPSIN_HIS; 1
DR DR PROSITE; PS00135; TRYPSIN_SER; 1
DR DR Blood coagulation; Plasma; Serine protease; Calcium-binding;
DR DR Hydrolase; Glycoprotein; 3D-structure.
FT FT NON TER      1
FT FT ACT_SITE     81
FT FT ACT_SITE    133
FT FT ACT_SITE    137
FT FT ACT_SITE    229
FT FT ACT_SITE    229
FT FT CARBOHYD     21
FT FT CARBOHYD    36
FT FT CARBOHYD   124
FT FT CARBOHYD   271
FT FT NON TER     271
SQ SQ SEQUENCE      271 AA; 29992 MW; 3DCI8B7FC6G6A24B CRC64;

Query Match          100.0%; Score 46; DB 1; Length 271;
Best Local Similarity 100.0%; Pred No 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVDRATCLR 9
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DB       194 LVDRATCLR 202

RESULT 2
FA9 SHEEP
ID ID_FA9SHEEP STANDARD; PRT; 274 AA.
IC P16291
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Annotation update)
DT F9 Coagulation factor IX (BC 3.1.2.25), (Christmas factor) (Fragment).
GN GN_Ovis aries (Sheep).
OS Ovis aries (Sheep).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
NCBI TaxId=9940
RP RESEQUENCE FROM N.A.
RX MEDLINE=90152675; PubMed=2303254;
RA Sarkar G., Koehler D.D., Sommer S.S.;
RR "Direct sequencing of the activation peptide and the catalytic domain
RT of the factor IX gene in six species.";
RL Genomics 6:133-143(1990).
CC CC -! FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF CALCIUM AND
CC CC LONGS, PHOSPHOLIPIDS, AND FACTOR VIII.
CC CC -! CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor x to
CC CC form factor xa.
CC CC -! SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa. WHICH EXCISES THE
CC CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY 13.
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CC CC ..... for details).
CC CC EMBL; M26233; AAA31520.1; .

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DR MEROPS; S01.214; .  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR00294; Vlk\_dep\_GLA.  
 DR SMART; SM00069; Trypsin\_SPC; 1.  
 DR SMART; SM00020; TYP SP; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; PARTIAL.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Plasma; Serine protease; Calcium-binding;  
 KW Hydrolyase; Glycoprotein.  
 FT ACT SITE 96 96 CHARGE RELAY SYSTEM.  
 FT ACT SITE 144 144 CHARGE RELAY SYSTEM.  
 FT ACT SITE 240 240 CHARGE RELAY SYSTEM.  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT NON TER 282 282  
 SQ SEQUENCE 282 AA; 31447 MW; 88B37B0A673BEC9 CRC64;  
 Query Match 100.0%; Score 46; DB 1; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATCLR 9  
 DB 205 LVDRATCLR 213

RESULT 4  
 ID PAS BOVIN STANDARD; PRT; 285 AA.  
 AC P16295;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor) (Fragment).  
 GN F9.  
 OS *Cavia porcellus* (Guinea pig).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricomorpha; Caviidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90152675; PubMed=2303254;  
 RA Sarkar G., Koerber D.D., Sommer S.S.;  
 RT Direct sequencing of the activation peptide and the catalytic domain  
 RL Genomics 6:133-143(1990).  
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT  
 CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY  
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++  
 CC IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-lle bond in factor X to  
 CC -1- SUBSTRATE: FACTOR IX.  
 CC -1- ACTIVATION PEPTIDE AND THIS PRODUCES A MOLECULE CONSISTING OF 2  
 CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
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 CC EMBL; M26237; AAA37037.1;  
 CC HSP; P16293; 1PFX.  
 DR MEROPS; S01.214; .

DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR00294; Vlk\_dep\_GLA.  
 DR SMART; SM00069; Trypsin\_SPC; 1.  
 DR SMART; SM00020; TYP SP; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; PARTIAL.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Plasma; Serine protease; Calcium-binding;  
 KW Hydrolyase; Glycoprotein.  
 FT ACT SITE 99 99 CHARGE RELAY SYSTEM.  
 FT ACT SITE 147 147 CHARGE RELAY SYSTEM.  
 FT ACT SITE 243 243 CHARGE RELAY SYSTEM.  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT NON TER 285 285  
 SQ SEQUENCE 285 AA; 32032 MW; 68B36DD317C11C60 CRC64;  
 Query Match 100.0%; Score 46; DB 1; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVDRATCLR 9  
 DB 208 LVDRATCLR 216

RESULT 5  
 ID PAS BOVIN STANDARD; PRT; 416 AA.  
 AC P16295;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).  
 GN F9.  
 OS *Bos taurus* (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Ruminantia; Ruminantia; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=80056619; PubMed=291916;  
 RA Katsuyama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,  
 RT Direct sequencing of the activation peptide and the catalytic domain  
 RL Genomics 6:133-143(1990).  
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA  
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++  
 CC IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-lle bond in factor X to  
 CC -1- SUBSTRATE: FACTOR IX.  
 CC -1- ACTIVATION PEPTIDE AND THIS PRODUCES A MOLECULE CONSISTING OF 2  
 CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
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 CC EMBL; M26237; AAA37037.1;  
 CC HSP; P16293; 1PFX.  
 DR MEROPS; S01.214; .









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 RT "Evidence for a prevalent dimorphism in the activation peptide of  
 RT human coagulation factor IX.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).  
 RL [3]
- RP SEQUENCE FROM N.A.  
 RP MEDLINE=84236100; PubMed=6329734;  
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,  
 RA Huddleston J.A., Brownlee G.G.;  
 RT "The gene structure of human anti-haemophilic factor IX.";  
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 RL [4]
- RP SEQUENCE FROM N.A.  
 RP MEDLINE=83220780; PubMed=6687940;  
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 RA Jaye M., de la Salle H., Schambach F., Ballard A., Kohli V.,  
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 RT synthetic oligonucleotide probe deduced from the amino  
 RT acid sequence of bovine factor IX.";  
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 RL [5]
- RP SEQUENCE OF 36-326 FROM N.A.  
 RP TISSUE=Liver;  
 RP MEDLINE=84300526; PubMed=6089357;  
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
 RT "Isolation and characterization of human factor IX cDNA:  
 RT identification of two distinct regional assignments.";  
 RT Somat. Cell Mol. Genet. 10:465-473(1984).  
 RL [6]
- RP SEQUENCE OF 230-359 FROM N.A.  
 RP MEDLINE=88127096; PubMed=3340835;  
 RA Stoflet E.S., Koehler D.B., Sarkar G., Sommer S.S.;  
 RT "Genomic amplification with transcript sequencing.";  
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 RL [7]
- RP SEQUENCE OF 444-461 FROM N.A.  
 RP MEDLINE=94054330; PubMed=8236150;  
 RA de la Salle H., Charmanier J.L., Baas M.J., Schwartz A.,  
 RA Wisel M.L., Grunbaum L., Cazenave J.-P.;  
 RT "A deletion located in the 3' non translated part of the factor IX  
 RT gene responsible for mild haemophilia B.";  
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 RL [8]
- RP SEQUENCE OF 47-461 (VARIANT NAGAYA).  
 RP MEDLINE=90078229; PubMed=2592373;  
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
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- RP HYDROXYLATION OF ASP-110.  
 RP MEDLINE=83308813; PubMed=6888526;  
 RA McMullen B.A., Fujikawa K., Kisiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens.";  
 RT Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RL [10]
- RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
 RP MEDLINE=78194509; PubMed=659613;  
 RA di Sciopio R.G., Kurachi K., Davie E.W.;  
 RT "Activation of human factor IX (Christmas factor)."  
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 RL [12]
- RP CALCULUM-BINDING DATA.  
 RP MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity  
 RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";  
 RT J. Biol. Chem. 259:5698-5704(1984).  
 RL [12]
- RP ERRATUM.  
 RP MEDLINE=97199336; PubMed=9047312;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
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 RL [13]
- RP SEQUENCE CLEARANCE SITE.  
 RP MEDLINE=86189947; PubMed=3009023;  
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
 RT "Defective propeptide processing of blood clotting factor IX caused  
 RT by mutation of arginine to glutamine at position -4.";  
 RT Cell 45:343-348(1986).  
 RL [14]
- RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RP MEDLINE=90062160; PubMed=2511201.  
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.,  
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 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RT J. Biol. Chem. 264:2020-2025(1989).  
 RL [15]
- RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RP MEDLINE=92388094; PubMed=1517205;  
 RA Nishimura H., Takao T., Hase S., Shimomishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue.";  
 RT J. Biol. Chem. 267:17520-17525(1992).  
 RL [16]
- RP PHOSPHORYLATION OF SER-114.  
 RA Harris R.J., Papac D.I., Tuong L., Smith K.J.;  
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 RL structure analysis, pp-50-50, Annecy (1996).  
 RL [18]
- RP POST-TRANSLATIONAL MODIFICATIONS.  
 RP MEDLINE=92057537; PubMed=1113752;  
 RA Harris R.J., Papac D.I., Tuong L., Smith K.J., Heiman-Patterson T.,  
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 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX.";  
 RT Blood 97:130-138(2001).  
 RL [19]
- RP STRUCTURE BY NMR OF 47-93.  
 RP MEDLINE=95229407; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
 RT binding region of factor IX by two-dimensional NMR spectroscopy.";  
 RT J. Biol. Chem. 270:7980-7987(1995).  
 RL [20]
- RP STRUCTURE BY NMR OF 47-93.  
 RP MEDLINE=90326078; PubMed=7547952;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
 RT domain of factor IX.";  
 RT Biochemistry 34:12126-12137(1995).  
 RL [21]
- RP STRUCTURE BY NMR OF 47-93.  
 RP MEDLINE=96279169; PubMed=8663165;  
 RA Freedman S.J., Stojetin M.D., Baleja J.D., Jacobs M., Furie B.C.,  
 RA Furie B.;  
 RT "Identification of the phospholipid binding site in the vitamin K-  
 RT dependent blood coagulation protein factor IX.";  
 RT J. Biol. Chem. 271:16227-16236(1996).  
 RL [22]
- RP STRUCTURE BY NMR OF 47-93.  
 RP MEDLINE=97199336; PubMed=9047312;

RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
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 RT "Refinement of the NMR solution structure of the  
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
 RT by a genetic algorithm." *Biochemistry* 36:2132-2138 (1997).  
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 CC [23]  
 RN STRUCTURE BY NMR OF 91-133.  
 RA MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
 RT "Sequence-specific 1H NMR assignments, secondary structure, and  
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 RT factor domain of human epidermal growth factor IX." *Biochemistry*  
 RL Biochemistry 30:7402-7409 (1991).  
 CC [24]  
 RN STRUCTURE BY NMR OF 92-130.  
 RA MEDLINE=93284090; PubMed=1304885;  
 RA Barton M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,  
 RA Tee A.G.D., Brownlee G.G., Campbell I.D.C.;  
 RT "Structure of a Ca(2+)-binding epidermal growth factor-like  
 RT human factor IX compared with EGF and TGF-alpha." *Protein*  
 RL Protein Sci. 1:81-90 (1992).  
 CC [25]  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
 RA MEDLINE=95330802; PubMed=7606779;  
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;  
 RT "The structure of a Ca(2+)-binding epidermal growth factor-like  
 RT human factor IX in the presence of calcium ions." *Cell* 82:131-141 (1995).  
 RL Cell 82:131-141 (1995).  
 CC [26]  
 RN MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 100.0%; Score 45; DB 1; Length 461;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9  
 DB 376 LVDRATCLR 384

RESULT 9  
 ID PA9 RABIT STANDARD; PRT; 275 AA.  
 AC P16292;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor) (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Legomorphae; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=90152675; PubMed=2303254; S;  
 RA Kottmann D., Kottmann D., Semmler S.;  
 RT "Structure of the factor IX gene in six species." *Genomics* 6:133-143 (1990).  
 RL Genomics 6:133-143 (1990).  
 CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT  
 CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY  
 CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++  
 CC AND FACTOR VIII.  
 CC -1- CATALYTIC ACTIVITY: hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE  
 CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2  
 CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

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 CC EMBL Outstation at the address given below (see http://www.isb-emb.ch/announce/  
 CC or send an email to license@isb-emb.ch).  
 CC -----  
 CC EMBL; M26234; AAA1251.1; .  
 DR HSSP; P16293; 1PFX.  
 DR MEROPS; S01.214; .  
 DR InterPro; IPR001254; Ser-Protease\_Try.  
 DR Pfam; PF000294; 1; MEROPS; S01.214; 1.  
 DR Pfam; PF00085; 1; MEROPS; S01.214; 1.  
 DR SMART; SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; PARTIAL.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Plasma; Serine protease; Calcium-binding;  
 FT NON TER 89 89 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 137 137 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 233 233 CHARGE RELAY SYSTEM.  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT NON TER 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 275 AA; 30776 MW; FE364489AC76BE87 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VDRATCLR 9  
 DB 199 VDRATCLR 206

RESULT 10  
 ID P40 ILTVT STANDARD; PRT; 586 AA.  
 AC P23984;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Capsid protein P40 (Contains: Capsid protein VP24 (Assemblin)  
 DE (Protease) (EC 3.4.21.97); Capsid protein VP22A (V892) (ILTV).  
 OS Infectioyogorachetivirus (strain thorax herpesviridae).  
 OC Alphaherpesvirinae; bird herpesviridae;  
 OC Infectioyogorachetis-like viruses.  
 OX NCBI\_TaxID=10344;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=90301509; PubMed=2163526;  
 RA Griffin A.M.;  
 RT "Sequence of the capsid p40 gene from infectious  
 RT laryngotracheitis virus." *Nucleic Acids Res.* 18:3664-3664 (1990).  
 RL Nucleic Acids Res. 18:3664-3664 (1990).  
 CC [2]  
 RN SEQUENCE OF 1-516 FROM N.A.  
 RA MEDLINE=90218031; PubMed=2157797;  
 RA Griffin A.M.; Bourneill J.S.;  
 RT "The sequence of DNA from the region of the  
 RT thymidine kinase gene of infectious laryngotracheitis virus;  
 RT potential evolutionary relationships between the herpesvirus  
 RT subfamilies." *J. Gen. Virol.* 71:841-850 (1990).  
 RL J. Gen. Virol. 71:841-850 (1990).  
 CC -1- FUNCTION: VP22A IS A COMPONENT OF PROGENY DNA. VP24 IS A PROTEASE  
 CC PROCESSING AND PACKAGING OF PROGENY DNA.



```

FT CARBOHYD 714 714 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 939 939 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 961 961 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1087 1087 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1090 1090 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1095 1095 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1211 1211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1272 1272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1330 1330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1428 1428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1474 1474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1565 1565 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1669 1669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1715 1715 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1738 1738 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2213 2213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2228 2229 N -> D (IN REF 2 AND 3).
FT CONFLICT 2246 2259 OC -> KS (IN REF 2 AND 3).
FT SEQUENCE 2347 AA; 26395 MW; E44FDFD410CIDA CRC64;
Query Match 72.94; Score 34; DB 1; Length 2347;
Basic Local Similarity 72.94; Score 34; DB 1; Length 2347;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 309 LVDEAHLR 317

RESULT 12
US59 HCWVA STANDARD; PRT; 123 AA.
ID P16746;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
GN UL59
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OC NCBI_TaxID=10360;
RN [1]
RN [2] SEQUENCE FROM N.A.
RN [3] MEDLINE=90269036; PubMed=2161319;
RA Choe M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hrachivac A.C. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston X.M., Barrell B.G.;
RA "Analysis of the protein-coding content of the sequence of human
RA cytomegalovirus strain AD169";
RA Curr. Top. Microbiol. Immunol. 154:125-169 (1990).
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Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 3 LVDEAHLR 11

RESULT 13
CFAD HUMAN STANDARD; PRT; 253 AA.
ID P00746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)
DE (Properdin factor D) (Adipsin)
DS DF.
GN Homo sapiens (Human)
OS Homo sapiens (Human)
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN [2] SEQUENCE OF 8-253 FROM N.A.
RN [3] MEDLINE=92250520; PubMed=1374388;
RA White R.T., Damm D., Hancock N., Rosen B.S., Lowell B.B., Usher P.,
RA Flier J.S., Spiegelman B.M.;
RA "Human adipon is identical to complement factor D and is expressed
RA at high levels in adipose tissue";
RA J. Biol. Chem. 267:9210-9213 (1992).
RN [2]
RN [3] SEQUENCE FROM N.A.
RN [4] Flier J.S., Spiegelman B.M., Rosen B.M.;
RN [5] Patent number WO9006365, 14-JUN-1990.
RN [6]
RN [7] SEQUENCE OF 26-252
RN [8] MEDLINE=950004; PubMed=6382466;
RA Niemann M.A., Brown A.S., Bennett J.C., Volanakis J.E.;
RA "Amino acid sequence of human D of the alternative complement
RA pathway.";
RA Biochemistry 23:2482-2486 (1984).
RN [4]
RN [5] PARTIAL SEQUENCE OF 26-252
RN [6] MEDLINE=950004; PubMed=6382466;
RA Niemann M.A., Brown A.S., Bennett J.C., Volanakis J.E.;
RA "Amino acid sequence of human factor D of the complement system.
RA Similarity in sequence between factor D and proteases of non-plasma
RA origin.";
RA FEBS Lett. 166:347-351 (1984).
RN [5]
RN [6] PARTIAL SEQUENCE OF 26-61 AND 194-220.
RN [7] MEDLINE=90269036; PubMed=2161319;
RA Choe M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hrachivac A.C. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston X.M., Barrell B.G.;
RA "Analysis of the protein-coding content of the sequence of human
RA cytomegalovirus strain AD169";
RA Curr. Top. Microbiol. Immunol. 154:125-169 (1990).
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RA Narayana S.V.L., Carlson M., El-Kabbani O., Kilpatrick J.M., Moore D.,  
 RA Chen X., Buga C.E., Volanakis J.E., Delucias L.J.: A  
 RT resolution of human factor D. A complement system protein at 2.0-A  
 J. Mol. Biol. 235:695-708 (1994).  
 [9]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=96025834; PubMed=7592653;  
 RA Kim S., Narayana S.V., Volanakis J.E.;  
 RA enhanced catalytic activity of complement factor D mutant expressing  
 RT the human factor D gene.  
 J. Biol. Chem. 270:24359-24405 (1995).  
 CC -!- FUNCTION: FACTOR D CLEAVES FACTOR B WHEN THE LATTER IS COMPLEXED  
 CC WITH FACTOR C3B, ACTIVATING THE C3BB COMPLEX, WHICH THEN BECOMES  
 CC THE C3 CONVERTASE OF THE ALTERNATE PATHWAY. ITS FUNCTION IS  
 CC HOMOLOGOUS TO THAT OF C1S IN THE CLASSICAL PATHWAY.  
 CC -!- CATALYTIC ACTIVITY: Cleaves component factor B (A9g-I-lys) when in  
 CC complex with component factor C3 (Cvf).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -!- CAUTION: IN ADDITION TO THE CONFLICTS SHOWN IN THE FEATURE TABLE,  
 CC REF. 3 SEQUENCE HAD A PEPTIDE IN THE WRONG ORDER AND ANOTHER ONE  
 CC MISSING.  
 -----  
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 CC EMBL; M44526; AAA3527.1; ALT\_INIT.  
 DR PIR; A40197; DBHD.98.  
 DR PDB; 1DST; 13-JUL-96.  
 DR PDB; 1DSU; 17-AUG-96.  
 DR MEROPS; S01.191; .  
 DR Genew; HGNC:2771; DF.  
 DR MIM; 134350; .  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR Pfam; PF0001254; Ser\_Protease\_Try.  
 DR PRINTS; PR007221; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Complement alternate pathway; plasma; Hydrolase; Serine protease;  
 FT SIGNAL; Glycoprotein; 2; Signal.  
 FT PROPEP 21 25 ACTIVATION PEPTIDE (POTENTIAL).  
 FT CHAIN 26 253 COMPLEMENT FACTOR D.  
 FT ACT\_SITE 66 66 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 112 112 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 208 208 CHARGE RELAY SYSTEM.  
 FT DISULFID 51 67  
 FT DISULFID 151 167  
 FT DISULFID 195 208  
 FT DISULFID 204 229  
 FT DISULFID 26 26  
 FT CONFLICT 35 35 H -> M (IN REF. 1).  
 FT CONFLICT 35 35 M -> F (IN REF. 6).  
 FT CONFLICT 40 40 H -> F (IN REF. 6).  
 FT CONFLICT 49 49 H -> E (IN REF. 4 AND 5).  
 FT CONFLICT 52 52 G -> A (IN REF. 1 AND 2).  
 FT CONFLICT 53 53 C -> T (IN REF. 1 AND 2).  
 FT CONFLICT 63 63 Q -> T (IN REF. 4).  
 FT CONFLICT 73 73 D -> G (IN REF. 4).  
 FT CONFLICT 83 86 HSLS -> THLP (IN REF. 3).  
 FT CONFLICT 83 84 HS -> ST (IN REF. 4).  
 FT CONFLICT 94 95 MISSING (IN REF. 4).  
 FT CONFLICT 96 96 D -> E (IN REF. 4).  
 FT CONFLICT 136 136 Q -> G (IN REF. 4).  
 FT CONFLICT 178 191 TGNRTHDGAITE -> KRLRYDVL (IN REF. 4).

FT CONFLICT 243 243 S -> T (IN REF. 3).  
 FT CONFLICT 250 250 S -> H (IN REF. 3).  
 FT CONFLICT 250 250 MISSING (IN REF. 4).  
 SQ SEQUENCE 253 AA; 2700 MW; 27004 MD; 805357/8053566AD CRC64;  
 Query Match 71.7%; Score 33; DB 1; Length 253;  
 Best Local Similarity 66.7%; Pred.No. 14;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LVDRATCLR 9  
 Db 173 VLDRATCLR 181  
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 RESULT 14  
 ID Y220\_HUMAN STANDARD; PRT; 546 AA.  
 CD 1926-CT-2003 (Sep. 40, Created)  
 DT 16-OCT-2001 (Sep. 40, Last sequence update)  
 DT 16-OCT-2001 (Sep. 40, Last annotation update)  
 DE Hypothetical protein KIAA0220.  
 GN KIAA0220.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]\_X2415-9606;  
 RN TISSUE=Bone marrow;  
 RC SEQUENCE FROM N.A.  
 RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,  
 RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
 RA "Prediction of the coding sequences of unidentified human genes. VI.  
 RA The 11th set of the clones, their gene structures, and RT-PCR  
 RT analysis of cDNA clones from cDNA line KG-1 and brain";  
 DNA Res. 3:321-329 (1996).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99425270; PubMed=10493829;  
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,  
 RA DeLuca J., Mason C.A., Rossy W.L., Karmali M., Cronin  
 RA DeLuca J., May, C.P., May, C.Y., May, C.Y., May, C.Y.,  
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
 RP "Genome duplications and other features in 12 Mb of DNA sequence from  
 RT human chromosome 16p and 16q";  
 RL Genomics 60:295-308 (1999).  
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 CC EMBL; D65974; BAA13210.1; ALT\_INIT.  
 DR EMBL; AC003007; AAC13670.1; .  
 DR EMBL; D65974; BAA13210.1; .  
 SQ SEQUENCE 546 AA; 60996 MW; F09D0824566CEP71 CRC64;  
 Query Match 71.7%; Score 33; DB 1; Length 546;  
 Best Local Similarity 66.7%; Pred.No. 29;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 LVDRATCLR 9  
 Db 75 LVHRTCLR 83  
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 RESULT 15  
 ID CLC2\_HUMAN STANDARD; PRT; 268 AA.

AC Q9895; Q9895; Q00765;  
 DT 16-OCT-2001 (Ref. 40, Created)  
 DT 16-OCT-2001 (Ref. 40, Last sequence update)  
 DT 16-OCT-2001 (Ref. 40, Last annotation update)  
 DT CTRC OR CLC Recursor (EC 3.4.21.2) (Chymotrypsin C).  
 GS Homo sapiens (Human).  
 OS  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 ON NCBI\_TaxID=9606;  
 RX  
 RP SEQUENCE FROM N.A., AND VARIANT TRP-80.  
 RP MEDLINE:94223265; PubMed:8635596;  
 RA Tomomura A., Akiyama K., Itoh H., Yoshino I., Tomomura M., Nishii Y.,  
 RA Nakura T., Saheki T.;  
 RA "Molecular cloning and expression of human caldecrin.";  
 RT PNAS Lett. 386:26-28(1996).  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RP CSDA11.C  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL (3)  
 RP SEQUENCE OF 17-268 FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Szegoleit A.;  
 RA "A human pancreatic chymotrypsin: biochemical and molecular  
 RT characterization.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RL (4)  
 RP CHARACTERIZATION.  
 RP MEDLINE:98207038; PubMed:9538241;  
 RA Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,  
 RA Saheki T.;  
 RT "Caldecrin is a novel-type serine protease expressed in pancreas, but  
 RT not in the pancreas of the rat.";  
 RT from calder. 123:546-554(1998).  
 RL J. Biochem. 123:546-554(1998).  
 CC 1- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC  
 CC ACTIVITY.  
 CC 1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa,  
 CC Pre-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Glu-|-Xaa, Asn-|-Xaa.  
 CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ELASTASE SUBFAMILY.  
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 CC -----  
 CC EMBL; S82198; AAB47104.2; ALT SEQ.  
 CC EMBL; AL031283; CAB77355.1; -;  
 CC EMBL; Y13697; CA474031.1; -;  
 CC HSSP; P00766; 1CHG.  
 CC MEROPS; S01157; -;  
 CC ChEMBL; CHEMBL123; -;  
 CC MIM; 601405; 2223; CTRC.  
 CC InterPro; IPR001314; Chymotrypsin.  
 CC InterPro; IPR001254; Ser. protease\_Try.  
 CC Pfam; PF00089; trypsin; 1.  
 CC PRINTS; P000722; chymotrypsin.  
 CC SMART; SM0020; TRYD\_SPC; 1.  
 CC PROSITE; PS00130; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00136; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;  
 KW Polymorphism.  
 FT SIGNAL.  
 FT PROPEP 17 16 POTENTIAL.  
 FT CHAIN 30 268 ACTIVATION PEPTIDE.  
 FT CALDECRIN.

FT ACT\_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 216 216 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 17 141 BY SIMILARITY.  
 FT DISULFID 19 225 BY SIMILARITY.  
 FT DISULFID 18 202 BY SIMILARITY.  
 FT DISULFID 212 243 BY SIMILARITY.  
 FT DISULFID 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARIANT 80 80 R->W.  
 FT CONFLICT 16 16 /FTIDAVAR\_010928.  
 FT CONFLICT 52 52 N->D (IN REF. 1).  
 FT CONFLICT 52 52 N->D (IN REF. 1).  
 SQ SEQUENCE 268 AA; 29484 MW; 450BF33BA496516F CRC64;  
 Query Match 69.6%; Score 32; DB 1; Length 268;  
 Best Local Similarity 66.7%; Pred. No. 23;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LVDRATCLR 9  
 DB 180 VDRATCLR 188  
 Search completed: May 6, 2003, 15:01:27  
 Job time : 10 secs

GenCore version 5.1.4 ps\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 14:59:05 ; Search time 15.75 seconds  
(without alignments)  
54,934 Million cell updates/sec

Title: US-09-851-422b-1

Perfect score: 46

Sequence: 1 LVDRATCLR 9

Scoring table: BLASTSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum E-value: 1000000000

Listing first 45 summaries

Database : PR73:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	271	2 146580	factor IX - pig (f
2	46	100.0	274	2 147078	coagulation factor
3	46	100.0	282	2 184621	coagulation factor
4	46	100.0	285	2 148144	coagulation factor
5	46	100.0	416	1 KFS90	coagulation factor
6	46	100.0	432	2 K30331	coagulation factor
7	46	100.0	432	2 K30331	coagulation factor
8	46	100.0	461	1 KFU913	coagulation factor
9	42	91.3	275	2 146712	factor IX - rabbit
10	36	78.3	586	1 A43675	capsid protein p40
11	36	78.3	909	2 H87729	protein Y23H5A.7
12	34	73.9	254	2 A49329	trypsin-like prote
13	34	73.9	434	2 A81977	citrate synthase
14	33	71.7	230	2 A40186	kinase-related pro
15	33	71.7	230	2 A40186	kinase-related pro
16	33	71.7	123	2 S09822	hypothetical prote
17	33	71.7	165	2 H83612	hypothetical prote
18	33	71.7	246	1 DBHU	complement factor
19	33	71.7	294	2 A49932	2,2',3'-triiodoxyb
20	33	71.7	997	2 A60776	230k bulbous pemph
21	32	69.6	362	2 H97253	deoxycytidylyl de
22	32	69.6	362	2 H97253	deoxycytidylyl de
23	32	69.6	268	2 S68825	pancreatic elastase
24	32	69.6	323	2 C30338	DNA transport mach
25	32	69.6	343	2 E86310	protein Fil3.6 [im
26	32	69.6	502	2 AE3601	periplasmic oligop
27	32	69.6	538	2 E84863	hypothetical prote
28	32	69.6	547	1 S28904	intercellular adhe
29	32	69.6	688	2 S39491	proteochlorophyllid

30 32 69.6 863 1 S51789  
31 32 69.6 2649 2 A40937  
32 31 69.6 128 2 A40937  
33 31 69.6 128 2 A40937  
34 31 69.6 130 2 A72720  
35 31 69.6 162 2 A75443  
36 31 69.6 286 2 F72599  
37 31 69.6 308 2 F95903  
38 31 69.6 378 2 A83278  
39 31 69.6 417 2 E70660  
40 31 69.6 431 2 E70660  
41 31 69.6 431 2 A56822  
42 31 69.6 498 2 J02353  
43 31 69.6 520 2 A13596  
44 31 69.6 543 2 B84398  
45 31 69.6 555 2 T43847

## ALIGNMENTS

RESULT 1  
146580  
Factor IX - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1999 #sequence\_revision 21-Feb-1997 #text\_change 22-Jun-1999  
R:Sartar, G.; Koebel, D.D.; Sommer, S.S.  
Genomics 6, 133-143, 1990  
A>Title: Direct sequencing of the activation peptide and the catalytic domain of the fa  
A:Reference number: 146580; MUID:90152675; PMID:2303254  
A:Accession: 146580  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Cross-references: GB:M26235; NID:q164450; PIDN:AAA1031.1; PID:q164451  
A:Superfamily: coagulation factor X; SCF homology; Gla domain homology; trypsin homology;  
F:45-271/Domain: trypsin homology (fragment) <TRY>

Query Match 100.0%; Score 46; DB 2; Length 271;  
Best Local Similarity 100.0%; Pred. No. 0.1; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9  
DB 194 LVDRATCLR 202

## RESULT 2

147078  
Ovis orientalis aries (domestic sheep)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C>Date: 15-Oct-1996 #sequence\_revision 15-Oct-1996 #text\_change 22-Jun-1999  
R:Sartar, G.; Koebel, D.D.; Sommer, S.S.  
Genomics 6, 133-143, 1990  
A>Title: Direct sequencing of the activation peptide and the catalytic domain of the fa  
A:Reference number: 147078; MUID:90152675; PMID:2303254  
A:Accession: 147078  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-274 <SAR>  
A:Cross-references: GB:M26233; NID:q165878; PIDN:AAA1520.1; PID:9552419  
A:Superfamily: coagulation factor X; SCF homology; Gla domain homology; trypsin homology;  
C:Keywords: hydrolase; serine proteinase  
F:45-274/Domain: trypsin homology (fragment) <TRY>

Query Match 100.0%; Score 46; DB 2; Length 274;  
Best Local Similarity 100.0%; Pred. No. 0.1; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9  
DB 194 LVDRATCLR 202







A>Note: 194-Thr was also found

R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.

J. Biol. Chem. 259, 5698-5704, 1984

A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site

A:Reference number: A37543; PMID:84185715; PMID:6425296

A:Contents: annotation; calcium binding

R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.

J. Biol. Chem. 260, 43754-43755, 1985

A:Reference number: A37544

A:Contents: annotation; calcium binding, correction

R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.

Cell 45, 343-348, 1986

A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation

A:Reference number: A37545; MUID:86189947; PMID:3009023

A:Contents: annotation; signal sequence cleavage site

J:Biochem. J. 244, 21267-21265, 1988

A>Title: Blood clotting factor IX

A:Reference number: A36422; MUID:90078229; PMID:2592373

A:Contents: annotation; sequence of mutant B(M) Nagoya

A:Reference number: A30622; MUID:90078229; PMID:2592373

A>Note: carboxylation, glycosylation, and cleavage sites

R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tee, A.G.D.; Brownlie, S.

submitted to the Brookhaven Protein Data Bank, November 1991

A:Contents: annotation; conformation by (1)H-NMR, residues 92-130

A>Note: recombinant form expressed in yeast

C:Comment: Factor IX is activated by factor Xla, which excises the activation peptide p.p. 1-10

C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K dependent modification

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with other amino acids, forms a stable complex

C:Genetics:

A:Gene: CDB:P9

A:Accession: GDB:113900; OMIM:306500

A:Map: position: 3q27.1-q27.2

A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1

C:Function:

A>Description: catalyzes the proteolytic activation of coagulation factor X in the presence of factor XI

A:Pathway: blood coagulation intrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; Carboxyglutamic acid; hydroxycarboxylic acid; proteinase; serine protease

F:128-46/Domain: propeptide status experimental <PPT>

F:31-91/Domain: Gla domain homology <GLA>

F:47-191/Product: coagulation factor IXa light chain status experimental <ALC>

F:97-128/Domain: EGF homology <BGI>

F:134-170/Domain: EGF homology <EG2>

F:192-226/Domain: activation peptide #status experimental <ACT>

F:227-246/Product: coagulation factor IXa heavy chain #status experimental <ANC>

F:27-30/Domain: propeptide status experimental <PPR>

F:53-64, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #Glu

F:64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-268, 382-396, 407-435/DNA

F:99/Binding site: carboxylate (Ser) (covalent) #status experimental

F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental

F:203-213/Binding site: carboxylate (Asn) (covalent) #status experimental

F:205-215/Binding site: carboxylate (Thr) (covalent) #status experimental

F:246-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 100.0%; Score 46; DB 1; Length 461;

Best Local Similarity 100.0%; Pred. NO. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9

DB 376 LVDRATCLR 384

RESULT 9

146712

factor IX - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Accession: F046712

C:Accession: F046712

C:Sarker, G.; Koerber, D.D.; Sommer, S.S.

Change 22-Jun-1999



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Query Match          73.9%  Score 34;  DB 1;  Length 2347;
Best Local Similarity 77.8%  Pred. No. 1.8e-02;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY 1 LVDRATCLR 9
   ||| |||
DB 309 LVDEARCLR 317

RESULT 15
I40186
hypothetical protein 1169b - Bacteroides fragilis
C:Species: Bacteroides fragilis
C:Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40186; S41295
R:Triun, S.; Hagsoud, A.; Keyeset, G.; Sebald, M.
Microbiology 141, 524-535, 1999
A:Reference number: I40186; EMBL:U04321 from Bacteroides, S-nitroimidazole resistance
A:Accession: I40186
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Reads: 1-70 <RES>
A:Cross-references: EMBL:X76949; NID:9440383; PID:CAA54271.1; PID:9440385

Query Match          71.7%  Score 32;  DB 2;  Length 70;
Best Local Similarity 82.5%  Pred. No. 1.2e-02;
Matches 5;  Conservative 3;  Mismatches 3;  Indels 0;  Gaps 0;

QY 1 LVDRATCLR 8
   :|:|:|
DB 57 MLDKATCLR 64

Search completed: May 6, 2003, 15:03:27
JOS time : 17.75 secs

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GenCore version 5.1.4.p5.457a  
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OW protein - protein search, using sw model

Run on: May 6, 2003, 15:01:10 | Search time 18 Seconds  
(without alignments)  
43.143 Million cell updates/sec

Title: US-09-851-422b-1

Perfect score: 46

Sequence: 1 LVDATCLR 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : \*

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubaa/US08\_NEW\_PUB.pcp.\*
- 2: /cgn2\_6/prodata/1/pubaa/PCT\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/prodata/1/pubaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/prodata/1/pubaa/US07\_NEW\_PUB.pcp.\*
- 5: /cgn2\_6/prodata/1/pubaa/US07\_PUBCOMB.pcp.\*
- 6: /cgn2\_6/prodata/1/pubaa/US07\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/prodata/1/pubaa/PCTUS\_PUBCOMB.pcp.\*
- 8: /cgn2\_6/prodata/1/pubaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/prodata/1/pubaa/US09\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/prodata/1/pubaa/US09\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/prodata/1/pubaa/US10\_NEW\_PUB.pcp.\*
- 12: /cgn2\_6/prodata/1/pubaa/US10\_PUBCOMB.pcp.\*
- 13: /cgn2\_6/prodata/1/pubaa/US60\_NEW\_PUB.pcp.\*
- 14: /cgn2\_6/prodata/1/pubaa/US60\_PUBCOMB.pcp.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	181	10	US-09-864-761-46600
2	46	100.0	461	9	US-10-132-829-5
3	46	100.0	461	9	US-09-848-708-3
4	46	100.0	461	9	US-09-848-708-3
5	33	71.7	101	9	US-10-012-542-351
6	33	71.7	208	10	US-09-821-255-2
7	32	69.6	44	12	US-10-001-843-188
8	32	69.6	252	9	US-09-864-761-35244
9	32	69.6	434	10	US-09-753-436-120
10	32	69.6	434	10	US-09-753-436-120
11	32	69.6	517	10	US-09-753-436-120
12	32	69.6	517	10	US-09-753-436-120
13	32	69.6	2125	9	US-09-919-172-29
14	31	67.4	24	9	US-10-012-542-362
15	31	67.4	223	10	US-09-870-162A-13
16	31	67.4	338	10	US-09-886-055-205
17	31	67.4	382	10	US-09-731-872-312
18	31	67.4	429	9	US-10-012-542-366
19	31	67.4	466	10	US-09-731-872-311

Sequence 365, App  
Sequence 17, Appl  
Sequence 1, Appl  
Sequence 660, App  
Sequence 2, Appl  
Sequence 10, Appl  
Sequence 4, Appl  
Sequence 626, App  
Sequence 626, App  
Sequence 34304, A  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 46, Appl  
Sequence 3, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 166, App  
Sequence 1749, Ap  
Sequence 1143, Ap  
Sequence 36732, A  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 14, Appl  
Sequence 2, Appl

20 31 67.4 470 9 US-10-012-542-365  
21 31 67.4 470 9 US-10-012-542-365  
22 31 67.4 470 9 US-10-012-542-365  
23 31 67.4 470 9 US-10-012-542-365  
24 30 65.2 315 9 US-09-925-297-660  
25 30 65.2 363 9 US-10-045-815-2  
26 30 65.2 374 9 US-10-255-817-10  
27 30 65.2 736 9 US-10-045-815-4  
28 29 63.0 80 9 US-10-092-154-626  
29 29 63.0 80 9 US-09-764-847-626  
30 29 63.0 80 9 US-09-764-847-626  
31 29 63.0 80 9 US-09-764-847-626  
32 29 63.0 80 9 US-09-764-847-626  
33 29 63.0 326 9 US-10-108-915-46  
34 29 63.0 459 9 US-09-759-595-3  
35 29 63.0 460 9 US-10-001-254-16  
36 29 63.0 460 9 US-10-001-254-16  
37 29 63.0 460 9 US-09-759-595-10  
38 29 63.0 460 9 US-09-759-595-10  
39 28 60.9 10 9 US-10-078-929-168  
40 28 60.9 36 9 US-09-572-4048-1749  
41 28 60.9 57 10 US-09-864-761-36792  
42 28 60.9 70 12 US-10-107-371-1  
43 28 60.9 75 9 US-10-104-755-12  
44 28 60.9 77 9 US-09-792-793A-14  
45 28 60.9 119 9 US-10-141-965-2

ALIGNMENTS

RESULT 1  
US-09-864-761-46600  
Sequence 46600: Application US/09864761  
Prod. No. US20020046763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
IDENTIFYING AND CLONING GENES  
FILE REFERENCE: Aconica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26/05/632,366  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30/US01/00666  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30/US01/00667  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30/US01/00664  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30/US01/00669  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30/US01/00665  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30/US01/00668  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30/US01/00663  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30/US01/00662  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30/US01/00661

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; LENGTH: 181
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL033403.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EST HUMAN HIT: T28608.1, EVALUE 3.00e-36
; OTHER INFORMATION: SWISSPROT HIT: P00740, EVALUE 1.00e-107
US-09-884-761-46600

Query Match 100.0%; Score 46; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Caps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9
DB 96 LVDRATCLR 104

RESULT 2
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Genentech R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-PAL170
; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/02/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match 100.0%; Score 46; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Caps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9
DB 376 LVDRATCLR 384

RESULT 3
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Mark
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18

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; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match 100.0%; Score 46; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Caps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9
DB 376 LVDRATCLR 384

RESULT 4
US-09-118-748-2
; Sequence 2, Application US/0918748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; FILE REFERENCE: PCT/US99/04000
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match 99.1%; Score 41; DB 10; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.6; Indels 0; Caps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 8
DB 330 LVDRATCLR 337

RESULT 5
US-09-542-351
; Sequence 351, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113

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? FEATURE:
? OTHER INFORMATION: MAP TO AL033378.6
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3

```

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN HEMT, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BLOOD, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN BV474, SIGNAL = 1.5  
OTHER INFORMATION: SWISSPROT HIT: P37743, EVALUE 6.90e-01  
OTHER INFORMATION: EST\_HUMAN HIT: AUI41284.1, EVALUE 5.00e-31  
US-09-864-761-35244

Query Match 59.6%; Score 32; DB 10; Length 83;  
Best Local Similarity 75.0%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 2 VDRATCLR 9  
DB 10 VGRSTCLR 17

RESULT 9  
US-10-117-323-38  
Sequence 38, Application US/10117323  
Publication No. US20030054993A1  
GENERAL INFORMATION:  
APPLICANT: Rancourt, Derrick E.  
TITLE OF INVENTION: SHILVH, Colleen W.  
FILE REFERENCE: 033337-005  
CURRENT APPLICATION NUMBER: US/10/117,323  
CURRENT FILING DATE: 2002-04-08  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: US 60/294,736  
PRIOR APPLICATION NUMBER: US 60/350,962  
PRIOR FILING DATE: 2002-01-25  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 252  
STRANDEDNESS: Mouse  
ORGANISM: Mouse  
US-10-117-323-38

Query Match 69.6%; Score 32; DB 9; Length 252;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LYDRATCLR 9  
DB 164 VDRATCSR 172

RESULT 10  
US-09-753-436-120  
Sequence 120, Application US/09753436  
Publication No. US200302293A1  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Vazeux, Rosemary  
TITLE OF INVENTION: ICAM-Related Materials and Methods  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
STREETS: 4300 Marshall, O'Toole, Gertstein, Murray & Borun  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.25  
FILING DATE: 2001-10-26  
PCT NUMBER: US/09/753,436  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/382,289  
FILING DATE:  
APPLICATION NUMBER: US 08/487,113  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA: US 08/286,754  
FILING DATE: 05-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/102,852  
FILING DATE: 05-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,266  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/894,061  
FILING DATE: 05-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/869,724  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA: US 07/827,689  
FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Joseph A., Jr.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 33282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 434 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
ORGANISM: linear  
MOLECULE TYPE: Protein  
US-09-753-436-120

Query Match 69.6%; Score 32; DB 10; Length 434;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDRATC 7  
DB 292 IDRATC 297

RESULT 11  
US-10-047-542-65  
Sequence 65, Application US/10047542  
Publication No. US200308367A1  
GENERAL INFORMATION:  
APPLICANT: LARRICK, JAMES W.  
APPLICANT: MYCOFF, KEITH L.  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
FILE REFERENCE: 030905.0004.C1P1  
CURRENT APPLICATION NUMBER: US 2001-10-26  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/1932  
PRIOR FILING DATE: 2001-04-28  
PRIOR APPLICATION NUMBER: 60/200,298  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 101



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 547
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Homo sapiens
US-10-047-542-65

Query Match
Best Local Similarity 69.6%; Score 32; DB 9; Length 547;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDRATC 7
DB 402 IDRATC 407

RESULT 12
US-09-753-436-1
; Sequence 1, US0100293A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAV-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; STRESSES: Morganhill, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,436
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA: US 08/102,852
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William H. Sieppel, Jr.
; REGISTRATION NUMBER: 659
; REFERENCE/DOCKET NUMBER: 633282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 547 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULES TYPE: protein
; FEATURES:
; NAME/KEY: protein
; LOCATION: 30..547
US-09-753-436-1

Query Match
Best Local Similarity 69.6%; Score 32; DB 10; Length 547;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDRATC 7
DB 402 IDRATC 407

RESULT 13
US-09-919-172-29
; Sequence 29, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: ANTIBODIES TO CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQUENCE ID NO: 1
; LENGTH: 2125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 3774181CD1
US-09-919-172-29

Query Match
Best Local Similarity 77.8%; Score 32; DB 10; Length 2125;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVDRTATCLR 9
DB 1946 LVDRTATCLR 1954

RESULT 14
US-10-012-542-362
; Sequence 362, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: 9A Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112

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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 512  
 ; CYPRESS: Stentin Ver. 2.0

; SEQ ID NO 362  
 ; LENGTH: 24

; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-012-542-362

Query Match: 67.4%; Score 31; DB 9; Length 24;  
 Bld/Local Similarity 75.0%; Patent No. 17;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVDRTACL 8

DB 12 LQDRASCL 19

# RESULT 15

US-09-870-162A-13

; Sequence 13, Application US/09870162A

; Patent No. US20020042118A1

; GENERAL INFORMATION:

; APPLICANT: Breinig, Sabine

; APPLICANT INVENTOR: Georg

; INVENTOR: Induced Proteins of Thauera aromatica

; FILE REFERENCE: BC1006 US DIV

; CURRENT APPLICATION NUMBER: US/09/870,162A

; CURRENT FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: 09/516914

; PRIOR FILING DATE: 2000-03-01

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Thauera aromatica

US-09-870-162A-13

Query Match: 67.4%; Score 31; DB 10; Length 223;

Bld/Local Similarity 75.0%; Patent No. 1:6e-03;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVDRTACL 9

DB 46 LITRAGCLR 54

Search completed: May 6, 2003, 15:04:52

Job time : 19.3333 secs





FILING DATE: June 9, 1993  
 CLASSIFICATION: 525  
 PROSECUTION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GALGANO & BURKE  
 REGISTRATION NUMBER: 30,735  
 TELEPHONE/DOCKET NUMBER: 128-7  
 TELEPHONE: (516) 582-6151  
 TELEFAX: (516) 582-6191  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 415 Amino Acids  
 TYPE: Amino Acid  
 TOPOLOGY: single  
 MOLECULE TYPE: unknown to applicant  
 HYPOTHETICAL: -  
 ANTI-SENSE:  
 ORGANISM:  
 INDIVIDUAL ISOLATE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 ISSUE:  
 PAGES:  
 DATE:  
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 415.

Query Match 100.0%; Score 46; DB 1; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 0.21; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9  
 DB 330 LVDRATCLR 338

RESULT 5  
 US-08-295-411-2  
 Sequence 2, Application US/08295411  
 Patent No. 5679639  
 GENERAL INFORMATION:  
 APPLICANT: Griffin, John H.  
 APPLICANT: Masters, Rolf M.  
 TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
 TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
 TITLE OF INVENTION: For Inhibiting Coagulation  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Office of Patent Counsel, The Scripps  
 ADDRESSEE: Research Institute  
 STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE:

APPLICATION NUMBER: US/08/295,411  
 FILING DATE: 22-AUG-1994  
 CLASSIFICATION: 530  
 PROSECUTION DATA:  
 APPLICATION NUMBER: US 07/793,989  
 FILING DATE: 18-NOV-1991  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 4,163  
 TELEPHONE/DOCKET NUMBER: TSK1263.OCI  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 415 amino acids  
 TYPE: Amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1..145  
 OTHER INFORMATION: /note= "Factor IX Light Chain"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 146..180  
 OTHER INFORMATION: /note= "Factor IX Activation  
 OTHER INFORMATION: Peptide"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 181..415  
 OTHER INFORMATION: /note= "Factor IX Heavy Chain"  
 US-08-295-411-2

Query Match 100.0%; Score 46; DB 1; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 0.21; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 LVDRATCLR 9  
 DB 330 LVDRATCLR 338

RESULT 6  
 US-08-955-471-2  
 Sequence 2, Application US/08955471  
 Patent No. 5987515  
 GENERAL INFORMATION:  
 APPLICANT: Griffin, John H.  
 APPLICANT: Masters, Rolf M.  
 TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
 TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
 TITLE OF INVENTION: For Inhibiting Coagulation  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Office of Patent Counsel, The Scripps  
 ADDRESSEE: Research Institute  
 STREET: 10666 No. 596875th Torrey Pines Road, TPC 8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE:

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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/295,411
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSRI263.0C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-6312
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 415 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1-145
/ OTHER INFORMATION: /note= "Factor IX Light Chain"
/
/ NAME/KEY: Region
/ LOCATION: 146-180
/ OTHER INFORMATION: /note= "Factor IX Activation
/ OTHER INFORMATION: Peptide"
/
/ NAME/KEY: Region
/ LOCATION: 181-415
/ OTHER INFORMATION: /note= "Factor IX Heavy Chain"
/
US-08-955-471-2
Query Match 100.0%; Score 46; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 330 LVDRATCLR 338

RESULT 7
US-08-766-288-1
/ Sequence 1, Application US/08766288
/ Patent No. 5965040
/ GENERAL INFORMATION:
/ APPLICANT: Hallahan, et al.
/ TITLE OF INVENTION: Factor IX - Polymeric Conjugates
/ TITLE OF INVENTION: Factor IX
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: GALGANO & BURKE
/ STREET: 300 Rabro Drive
/ CITY: Hauppauge
/ STATE: New York
/ COUNTRY: USA
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb Storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS 6.0
/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/766,288
/ FILING DATE: June 8, 1993
/ CLASSIFICATION: 525
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/073,531
/ FILING DATE: June 8, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GALGANO & BURKE

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/ REGISTRATION NUMBER: 30,735
/ REFERENCE/DOCKET NUMBER: 128-7 (DIV)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 582-6161
/ TELEFAX: (516) 582-6191
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 415 Amino Acids
/ TYPE: Amino Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Unknown to applicant
/ MOLECULE TYPE: -
/ HYPOTHETICAL: -
/ ANTI-SENSE: -
/ ORIGINAL SOURCE:
/ ORGANISM:
/ INDIVIDUAL ISOLATE:
/ CELL TYPE:
/ IMMEDIATE SOURCE:
/ CLONING:
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE: JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATES:
/ RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 415.
/
US-08-766-288-1
Query Match 100.0%; Score 46; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LVDRATCLR 9
DB 330 LVDRATCLR 338

RESULT 8
PCT-US92-10242-2
/ Sequence 1, Application PCT/US9210242
/ GENERAL INFORMATION:
/ APPLICANT: Griffin, John H.
/ APPLICANT: Meesters, Rolf
/ TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/ TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
/ TITLE OF INVENTION: For Inhibiting Coagulation
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Office of Patent Counsel, The Scripps
/ ADDRESSEE: Research Institute
/ STREET: 10666 North Torrey Pines Road, TPC 8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10242
/ FILING DATE: 19921118
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas

```

```

: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SC80472P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 415 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1-145
: OTHER INFORMATION: /note= "Factor IX Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 146-180
: OTHER INFORMATION: /note= "Factor IX Activation
: OTHER INFORMATION: Peptide"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 181-415
: OTHER INFORMATION: /note= "Factor IX Heavy Chain"
: PCT-US92-10342-2
:
: Query Match 100.0%; Score 46; DB 5; Length 415;
: Best Local Similarity 100.0%; Pred. No. 0.21; 0; Indels 0; Gaps 0;
: Matches 9; Conservative 0; Mismatches 0;
:
: QY 1 LVDRATCLR 9
: DB 330 LVDRATCLR 338
:
: RESULT 9
: US-08-742-877-2
: Sequence 2, Application US/08742877
: Patent No. 6046380
: GENERAL INFORMATION:
: APPLICANT: CLARK, Anthony J.
: TITLE OF INVENTION: DNA SEQUENCES
: NUMBER OF SEQUENCES: 14
: CORRESPONDING PCT:
: ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: ZIP: 20005-3934
: COUNTRY: USA
: COMPLETION DATE: 03-NOV-1996
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/742,877
: FILING DATE: 01-NOV-1996
: CLASSIFICATION: 435
: PRIORITY INFORMATION:
: APPLICATION NUMBER: GB 9408717.8
: FILING DATE: 03-MAY-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: FLESHNER, RAZ E.
: REGISTRATION NUMBER: 34,331
: REFERENCE/DOCKET NUMBER: 0623-0470001/REF
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2500
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 461 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-742-877-2
:
: Query Match 100.0%; Score 46; DB 3; Length 461;
: Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;
: Matches 9; Conservative 0; Mismatches 0;
:
: QY 1 LVDRATCLR 9
: DB 376 LVDRATCLR 384
:
: RESULT 10
: US-09-053-871A-21
: Sequence 21, Application US/09053871A
: Patent No. 6315995
: GENERAL INFORMATION:
: APPLICANT: Pinsky, David J.
: APPLICANT: Stern, David
: APPLICANT: Solomon, Robert A.
: APPLICANT: Schmidt, Ann Marie
: TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
: TITLE OF INVENTION: STROKE OUTCOME
: FILE REFERENCE: 51917-B
: CURRENT APPLICATION NUMBER: US/09/053,871A
: CURRENT FILING DATE: 1998-04-01
: NUMBER OF SEQ NOS: 42
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 21
: LENGTH: 461
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-053-871A-21
:
: Query Match 100.0%; Score 46; DB 4; Length 461;
: Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;
: Matches 9; Conservative 0; Mismatches 0;
:
: QY 1 LVDRATCLR 9
: DB 376 LVDRATCLR 384
:
: RESULT 11
: 5521070-2
: Patent NO. 5521070
: APPLICANT: MEULIEN, PIERRE
: TITLE OF INVENTION: DNA SEQUENCE CODING FOR HUMAN FACTOR
: IX OR A SIMILAR PROTEIN, EXPRESSION VECTOR, TRANSFORMED CELLS,
: METHOD FOR PREPARING FACTOR IX AND CORRESPONDING PRODUCTS OBTAINED
: FROM SUCH CELLS
: NUMBER OF SEQUENCES: 6
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/209,489
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 970,966
: FILING DATE: 03-NOV-1992
: PRIORITY INFORMATION:
: APPLICATION NUMBER: 3,276
: FILING DATE: 08-NOV-1989
: SEQ ID NO: 2
: LENGTH: 461
: 5521070-2
:
: Query Match 100.0%; Score 46; DB 6; Length 461;
: Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;
: Matches 9; Conservative 0; Mismatches 0;
:
: QY 1 LVDRATCLR 9
: DB 376 LVDRATCLR 384

```

Db 376 LVDRATCLR 384

RESULT 12  
US-08-944-483-44

Patent No. 6232456 Application US/08944483

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANOOS, EDWARD N.

APPLICANT: HARRIS, MICHAEL C.

APPLICANT: RUSSELL, MICHAEL C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

TITLE OF INVENTION: OF THE PROSTATE

CORRESPONDENCE ADDRESS:

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER: IBM COMP.

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE: JUN. 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

TELEPHONE: 847/935-1729

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 228 amino acids

STANDARD: amino acid

STANDARD: amino acid

TOPOLOGY: linear

MOLECULE TYPE: No. 6232456e

US-08-944-483-44

Query Match 71.7%; Score 33; DB 4; Length 228;

Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9

DB 148 VLDRATCLR 156

RESULT 13

5223425-5

Patent No. 5223425

APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,

BARRY M.; WHITE, TYLER R.

TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT

D ACTIVITY

NUMBER OF SEQUENCES: 19

EJ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/277,963

FILING DATE: 30-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 34,203

FILING DATE: 02-APR-1987

SEQ ID NO: 5;

LENGTH: 238

5223425-5

Query Match 71.7%; Score 33; DB 6; Length 238;

Best Local Similarity 66.7%; Pred. No. 38;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9

DB 158 VLDRATCLR 166

RESULT 14

5223425-4

Patent No. 5223425

APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,

BARRY M.; WHITE, TYLER R.

TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT

D ACTIVITY

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/277,963

FILING DATE: 30-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 34,203

FILING DATE: 02-APR-1987

SEQ ID NO: 4;

LENGTH: 250

5223425-4

Query Match 71.7%; Score 33; DB 6; Length 250;

Best Local Similarity 66.7%; Pred. No. 40;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9

DB 170 VLDRATCLR 178

RESULT 15

5223425-8

Patent No. 5223425

APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,

BARRY M.; WHITE, TYLER R.

TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT

D ACTIVITY

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/277,963

FILING DATE: 30-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 34,203

FILING DATE: 02-APR-1987

SEQ ID NO: 8;

LENGTH: 253

5223425-8

Query Match 71.7%; Score 33; DB 6; Length 253;

Best Local Similarity 66.7%; Pred. No. 40;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVDRATCLR 9

DB 173 VLDRATCLR 181



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Job time : 16.4 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4.P5.4578  
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 14:57:44 ; Search time 40.95 Seconds  
(without alignments)  
29.286 Million cell updates/sec

Title: US-09-851-422b-1

Perfect score: 46

Sequence: 1 LVDRATCLR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID82/gcgdata/genesepc/genesepc-emb1/AA1981.DAT.\*  
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7: /SID82/gcgdata/genesepc/genesepc-emb1/AA1985.DAT.\*  
8: /SID82/gcgdata/genesepc/genesepc-emb1/AA1986.DAT.\*  
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23: /SID82/gcgdata/genesepc/genesepc-emb1/AA2001.DAT.\*  
24: /SID82/gcgdata/genesepc/genesepc-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	182	22	peptide #3514 enco
2	46	100.0	182	22	peptide #3514 enco
3	46	100.0	182	22	Human Factor-IX
4	46	100.0	415	14	Human Factor-IX
5	46	100.0	415	14	Factor IX (IX), H
6	46	100.0	454	16	Human Factor-IX
7	46	100.0	456	5	Part of the sequen
8	46	100.0	461	6	Sequence encoded b
9	46	100.0	461	6	Sequence of human
10	46	100.0	461	6	Sequence of human

11	46	100.0	461	11	AA05393	Mutant human facto
12	46	100.0	461	11	AA05394	Human Factor IX pr
13	46	100.0	461	11	AA05395	Human Factor IX pr
14	46	100.0	461	22	AA01028	Human wild-type fa
15	46	100.0	461	22	AA01028	Human Factor IX (h
16	46	100.0	461	23	AA021524	Protein of human f
17	46	100.0	461	23	AA021524	Human Factor IX.
18	46	100.0	461	23	AA050568	Recombinant human
19	41	89.1	415	12	AA010868	Amino acid sequenc
20	34	73.9	36	4	AA010868	Human Factor IX
21	34	73.9	36	4	AA010868	Human Factor IX
22	34	73.9	36	20	AA011751	Human Factor IX
23	34	73.9	36	20	AA011751	Human Factor IX
24	34	73.9	158	12	AA011721	ENY93/HTLV-1-IIIB'
25	33	71.7	96	22	AA014883	Novel bone marrow
26	33	71.7	101	21	AA0166427	Human gene 31-enco
27	33	71.7	138	20	AA013395	HEV peptide z12-or
28	33	71.7	205	22	AA047245	Protonibacterium
29	33	71.7	250	11	AA050521	Human Factor IX
30	33	71.7	250	11	AA050521	Human Factor IX
31	33	71.7	345	22	AA050572	Human adipisin gene
32	33	71.7	345	22	AA050572	Drosophila melanog
33	33	71.7	575	22	AA039439	Human polypeptide
34	33	71.7	581	22	AA011366	Human KIRAA0220 pr
35	33	71.7	581	22	AA011366	Human polypeptide
36	33	71.7	877	22	AA026284	Drosophila melanog
37	33	71.7	1374	22	AA011235	Novel human diagn
38	32	69.6	12	14	AA030472	ICAM-3 peptide fra
39	32	69.6	38	22	AA090306	Human immune/haema
40	32	69.6	83	22	AA029363	Peptide #2043 enco
41	32	69.6	83	22	AA029363	Peptide #2043 enco
42	32	69.6	83	22	AA019946	Protein #1945 enco
43	32	69.6	83	22	AA019946	Human brain expres
44	32	69.6	83	22	AA019946	Human brain expres
45	32	69.6	83	22	AA015530	Peptide #1984 enco

#### ALIGNMENTS

RESULT 1  
AB019008  
ID ABB36008 standard; Peptide; 181 AA.  
AC ABB36008;  
XX  
XX  
04-FEB-2002 (first entry)  
DT XX  
DT Peptide #3514 encoded by human foetal liver single exon probe.  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
OS Homo sapiens.  
XX  
XX WO200157277-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001, 2001WO-US00669.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0609408.  
XX 23-AUG-2000; 2000US-0532366.  
XX 27-SEP-2000; 2000US-0234359.  
XX 04-OCT-2000; 2000US-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI, 2001-483447/52.



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FT	/note= "gamma-carboxyglutamic acid"	
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FT	/label= OTHER	
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FT	Modified-site	
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FT	/note= "gamma-carboxyglutamic acid"	
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FT	Disulfide-bond	
FT	55..69	
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FT	333..347	
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FT	358..386	
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FT	17..127	EGF-like_region
FT	128..195	Region
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FT	155	
FT	Modified-site	
FT	/note= "PEG attachment site"	
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FT	Modified-site	
FT	/note= "PEG attachment site"	
FT	178..179	
FT	Cleavage-site	
FT	/note= "Factor Xia cleavage site"	
FT	196..412	
FT	Domain	
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XX		
XX	W09429370-A.	
PN	XX	
XX	22-DEC-1994.	
XX	07-JUN-1994.	
PF	XX	94W-USO6388.
XX	08-JUN-1993.	93US-0073531.
PR	(ENZO)- ENZON INC.	
PA	Gilbert CW, Hallahan TW;	
XX	WPI; 1995-036423/05.	
XX	New Factor IX-non-antigenic polymer conjugates - use	
FT	treatment of haemophilia B	
FT	Disclosure; Fig. 1; 27pp; English.	
XX	Human Factor-IX is a single chain glycoprotein having	
CC	given in AAS64265. Conjugates of Factor-IX with poly	
CC		

XX Disclosure; Page 126-128; 149pp; English.

XX The PC polypeptides indicated in the Features Table inhibit

XX coagulation (they prevent binding of serine protease to natural

XX substrates) to give rise to fibrinogen and intravascular blood

XX clots. SEQ ID NO 5-11 are from NCIB No. 11749.

CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described

CC in the specification but have not yet been added to the SEQUENCE

CC LISTING.

XX

XX Sequence 415 AA;

XX

Query Match

Best Local Similarity 100.0%; Score 46; DB 14; Length 415;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVDRATCLR 9

DB 330 LVDRATCLR 338

|||||

RESULT 5

AA67710

ID AAR67710 standard; Protein; 454 AA.

XX

XX AAR67710;

XX

XX 20-JUL-1995 (first entry)

XX

XX Human Factor-IX.

DE

KW Factor-IX; blood-clotting; hemophilia B; gene therapy;

KW adenovirus; vector.

KX

OS Homo sapiens.

PN W09429471-A.

XX

XX 22-DEC-1994.

XX

XX 13-APR-1994; 94MO-US04075.

XX

XX 10-JUN-1993; 93US-0074920.

XX

XX 25-MAR-1994; 94US-0218333.

XX

XX (GENE-) GENETIC THERAPY INC.

XX

XX Connolly S, Kaleko M, Smith T;

XX

XX WPI, 1995-036495/05.

XX

XX N-PSDB; AAQ601.

XX

XX New adenoviral vectors for treatment of haemophilia - contg. a

XX DNA sequence encoding a clotting factor, partic. Factor VIII or

XX Factor IX

XX

XX Disclosure; Fig. 11A-11B; 116pp; English.

XX

XX Human Factor-IX was used to construct recombinant adenovirus vectors

XX that produced therapeutic levels of the clotting factor when

XX administered to an animal host, potentially providing hemophilia B

XX gene therapy.

XX

XX Sequence 454 AA;

XX

Query Match

Best Local Similarity 100.0%; Score 46; DB 16; Length 454;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVDRATCLR 9

DB 369 LVDRATCLR 377

|||||

RESULT 6

AA67710

ID AAR67710 standard; Protein; 456 AA.

XX

XX AAR67710;

XX

XX 11-FEB-1992 (first entry)

XX

XX Part of the sequence of human factor IX.

XX

XX Christmas disease; therapy; haemophilia; factor IX; blood clotting;

XX diagnosis.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

XX Peptide 1..41

XX Protein 42..456

XX W08400560-A.

XX

XX 16-FEB-1984.

XX

XX 03-AUG-1983; 83WO-G800191.

XX

XX 06-MAY-1983; 83GB-0012491.

XX

XX 04-AUG-1982; 82GB-0022485.

XX

XX (NATR ) NATIONAL RES DEV CORP.

XX

XX (BROW/) BROWNLEE G G.

XX

XX Brownlee G, Choo KH;

XX

XX WPI, 1984-049331/08.

XX

XX N-PSDB; AAU60142.

XX

XX Recombinant DNA cloning vehicles - useful in prodn. of factor IX

XX polypeptide and of diagnostic probes for Christmas disease

XX

XX Example; Fig 9; 71pp; English.

XX

XX The inventors claim DNA molecules comprising part or all of the

XX human factor IX DNA. The invention also includes cDNA derived from

XX human factor IX RNA. Specifically claimed are: recombinant DNA (the

XX phage present in clone lambda HIX-1) deposited as NCIB No. 11749;

XX Recombinant DNA in which the cloning vehicle is the modified pAT 153

XX plasmid present in E.coli NCIB No. 11747; Recombinant DNA in which

XX the bovine factor IX DNA sequence is contained in the recombinant

XX DNA transformed into E.coli to form a clone deposited as NCIB No.

XX 11748.

XX

XX Sequence 456 AA;

XX

Query Match

Best Local Similarity 100.0%; Score 46; DB 5; Length 456;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVDRATCLR 9

DB 371 LVDRATCLR 379

|||||

RESULT 7

AA67710

ID AAR67710 standard; Protein; 456 AA.

XX

XX AAR67710;

XX

XX 13-FEB-1992 (first entry)

XX

XX Sequence encoded by part of the sequence of human factor IX cDNA.









XX PD 27-SEP-2001.

XX XX 21-MAR-2001; 2001WO-EP03220.

XX XX 22-MAR-2000; 2000SP-0106225.

PR 08-MAY-2000; 2000US-203249P.

XX XX (OCTA-) OCTAGENE GNBH.

XX XX Hauser C, Hoerster A, Schroeder C, Lehnerer W;

PI WPI, 2001-500175/66.

DR N-ESDB; AAD18173.

XX XX Recombinant producing human blood coagulation factors VIII and IX for

PT use in treating hemophilia -

PT xx Claim 21; Page 73-74; 104pp; English.

PS The present invention relates to an improved method for the production

CC of recombinant human blood clotting factors, especially factors VIII and

CC IX, using an immortalised cell line stably expressing viral transcription

CC activators and carrying a vector comprising a promoter and a sequence

CC encoding the blood coagulation factor. The factor VIII mutin or a gene

CC transfer vector is used in the preparation of agents for treating

CC haemophilia, especially haemophilia A. The present sequence is human

CC wild-type factor IX protein encoded by vector pGf36h9g.

XX XX Sequence 461 AA;

XX XX Query Match 100.0%; Score 46; DB 22; Length 461;

XX XX Best Local Similarity 100.0%; Pred. No. 1.1;

XX XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9

DB 376 LVDRATCLR 384

RESULT 15

AAB60281

D AAB60281 standard; Protein; 461 AA.

XX XX AAB60281;

AC AAB60281;

XX XX 30-MAR-2001 (first entry)

DT DT Human factor IX (hFIX) protein.

DE XX Age-related gene regulation; liver-specific; gene expression;

XX XX human factor IX; hFIX; ABE3; ABE3; ABE3; ABE3; ABE3; ABE3; ABE3;

XX XX antisenese therapy; gene therapy; thrombosis; cardiovascular disease;

KW diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;

KW osteoarthritis; dementia.

OS Homo sapiens.

XX XX WO2000075279-A2.

XX XX 14-DEC-2000.

PD PD

XX XX 06-JUN-2000; 2000WO-US15728.

PP 09-JUN-1999; 99US-0328925.

PR (UNWI ) UNIV MICHIGAN.

XX XX Kurachi K, Kurachi S;

PI WPI; 2001-061708/07.

DR N-ESDB; AAF54018.

XX XX

PT New regulatory elements that control age-related gene expression,

PT useful in gene therapy and for reducing factor IX expression -

XX Disclosure; Fig 8A-5; 25pp; English.

XX The invention relates to nucleic acid sequences which regulate gene

XX expression in an age-related manner and/or in a liver-specific manner.

CC The invention identifies regions of the human factor IX (hFIX) gene, and

CC a region of the human protein C (hPC) gene, which are age-related

CC regulatory sequences. The hFIX age-related regulatory sequences are

CC designated ABE3' (AAB54016) and ABE3' (AAB54017) and are found in the 5'

CC UTR (at position 2164-2165 of AAB54016) and 3' UTR (at position

CC 2164-2165 of AAB54017) respectively. The ABE3' and ABE3' sequences

CC to increase hFIX levels over the lifespan of an individual, however, they

CC can independently exert effects on hFIX mRNA in an age-related manner,

CC with ABE3' acting to stabilise hFIX mRNA, and ABE3' acting to increase hFIX

CC mRNA levels, over time. ABE3' also directs liver-specific expression. The

CC hPC gene age-related regulatory sequence is found in the 5' UTR

CC (AAB54081), and contains two PEA-3 (polyoma virus activator 3) elements

CC 5'-GAGGAA-3' and 5'-CAGGAG-3'. The age-related regulatory sequences of

CC the hPC gene are used to regulate gene expression in a liver-specific manner

CC by using in the construction of recombinant expression vectors for the

CC expression of a desired sequence in an age-related fashion in a host

CC cell. Preferred target genes for expression in such age-regulatable

CC expression vectors include those encoding proteins involved in blood

CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the

CC anti-coagulants protein C and antithrombin III), human

CC alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as

CC luciferase. The expression vectors include the human factor IX promoter, the

CC the T3 promoter and the SP6 promoter. The expression vectors of the

CC invention may be used in gene therapy to provide age- related and/or

CC liver-specific expression of target genes. Age-regulatable constructs may

CC be used in the treatment of such age-related conditions such as

CC thrombosis, cardiovascular disease, diabetes, Alzheimer's disease,

CC Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia.

CC Sequences of the human factor IX gene, the human factor IX promoter, the

CC treatment of thrombotic conditions associated with the natural

CC age-related rise in factor IX expression. Transgenic cells or animals

CC that contain vectors of the invention are useful as models of these

CC diseases, in screening for potential therapeutic agents and for studying

CC normal processes such as ageing and gene expression. Fragments and

CC homologues of age-related regulatory sequences, are useful as probes to

CC detect tissues or identify other such sequences in samples. The present

XX sequence represents hFIX.

XX XX Sequence 461 AA;

XX XX Query Match 100.0%; Score 46; DB 22; Length 461;

XX XX Best Local Similarity 100.0%; Pred. No. 1.1;

XX XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVDRATCLR 9

DB 376 LVDRATCLR 384

Search completed: May 6, 2003, 15:01:01

Job time : 42.95 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 14:59:45 ; Search time 14.2 seconds  
(without alignments)  
59.041 Million cell updates/sec

Title: US-09-851-422B-2

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Scoring table: BLOSUM62  
Gapop 10.0, Gspxt 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 21.\*

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.invertebrate.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.potent.\*
- 12: sp.truebacte.\*
- 13: sp.virus.\*
- 14: sp.unclassified.\*
- 15: sp.virus.\*
- 16: sp.bacteriap.\*
- 17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score at least as high as the best hit being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	25	10 P82952	P82952 prunus dulc
2	20	100.0	27	12 Q91R86	Q91R86 hepatitis c
3	20	100.0	31	1 QX254	QX254 halobacteri
4	20	100.0	45	3 Q9UG8	Q9UG8 rhizomucor
5	20	100.0	46	2 Q9S604	Q9S604 escherichia
6	20	100.0	48	16 Q8XWT7	Q8XWT7 raietonia s
7	20	100.0	49	10 Q9LJS3	Q9LJS3 arabidopsis
8	20	100.0	53	13 Q9QXF3	Q9QXF3 coturnix co
9	20	100.0	63	12 Q9S240	Q9S240 strigamoid
10	20	100.0	63	12 Q85240	Q85240 strigamoid
11	20	100.0	63	17 Q8H075	Q8H075 lactococcus
12	20	100.0	64	9 Q9ATU9	Q9ATU9 lactococcus
13	20	100.0	64	10 Q8WQJ3	Q8WQJ3 oryza sativ
14	20	100.0	64	16 Q9CFP1	Q9CFP1 lactococcus
15	20	100.0	66	4 Q9ATN6	Q9ATN6 homo sapien
16	20	100.0	67	16 Q9L6P7	Q9L6P7 salmonella

17	20	100.0	67	16 Q8X3Y5	Q8X3Y5 escherichia
18	20	100.0	73	16 Q9LJL1	Q9LJL1 streptomyce
19	20	100.0	83	4 Q9R86	Q9R86 homo sapien
20	20	100.0	84	16 Q9R86	Q9R86 homo sapien
21	20	100.0	84	16 Q9R86	Q9R86 rhizobium 1
22	20	100.0	85	9 Q9B054	Q9B054 mycobacteri
23	20	100.0	86	17 Q9HL23	Q9HL23 thermoplas
24	20	100.0	87	16 Q9PD28	Q9PD28 xyella fas
25	20	100.0	87	16 Q8XW88	Q8XW88 raietonia s
26	20	100.0	91	12 Q9S604	Q9S604 streptomyce
27	20	100.0	91	12 Q9S604	Q9S604 streptomyce
28	20	100.0	91	16 Q9KDH8	Q9KDH8 bacillus ha
29	20	100.0	92	2 Q88153	Q88153 rhizobium e
30	20	100.0	94	4 Q9GJH8	Q9GJH8 homo sapien
31	20	100.0	97	10 Q8VZ93	Q8VZ93 arabidopsis
32	20	100.0	99	10 Q8S916	Q8S916 oryza sativ
33	20	100.0	100	11 Q54945	Q54945 mus musculu
34	20	100.0	101	16 Q9KX18	Q9KX18 streptomyce
35	20	100.0	102	16 Q9KX18	Q9KX18 streptomyce
36	20	100.0	103	10 Q8S075	Q8S075 oryza sativ
37	20	100.0	103	12 Q9S619	Q9S619 human astri
38	20	100.0	104	10 Q9AUP1	Q9AUP1 oryza sativ
39	20	100.0	108	5 Q9V4G6	Q9V4G6 drosophila
40	20	100.0	111	2 Q9RIS9	Q9RIS9 streptococc
41	20	100.0	111	16 Q9RYK3	Q9RYK3 anabaena sp
42	20	100.0	112	12 Q8S916	Q8S916 hepatitis c
43	20	100.0	113	2 Q9LJL1	Q9LJL1 streptomyce
44	20	100.0	115	11 Q64186	Q64186 cavia (guin
45	20	100.0	115	16 Q984W4	Q984W4 rhizobium 1

#### ALIGNMENTS

RESULT 1  
ID P82952 PRELIMINARY; PRF; 25 AA.  
AC P82952;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
SE Seed alignment (protein fragment)  
CD 12 Seed alignment (protein fragment)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucotsids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
RN NCBI\_TaxID=3755;  
RX (1)  
RP SEQUENCE  
RC POLYMER: GENCO, TISSUE-SEED;  
RC Poltronieri P, Cappello M.S., Dobmae N., Conti A., Zacheo G.;  
RT Identification of igf-binding proteins as 2S albumin and conglutin in  
RT almond (Prunus dulcis) seed.";  
RL Submitted (FEB-2001) to the SWISS-PROT data bank.  
RC FUNCTION: MAY FUNCTION AS SEED STORAGE PROTEINS. HAS AN IGF-  
CC BINDING ACTIVITY.  
CC SUCTION CLEAR LOCATION: CYTOPLASMIC.  
CC SEED STORAGE PROTEIN.  
CC DEVELOPMENTAL STAGE: EXPRESSED DURING SEED MATURATION.  
KW Allergen: IGF-binding protein; Seed storage protein.  
FT NON TER 25 25  
SQ SEQUENCE 25 AA; 2872 MW; A04173DC65B48C99 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 25;  
Best Local Similarity 100.0%; Ref. No. 49;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRAT 4  
DB 21 DRAT 24

RESULT 2

Q51K66 PRELIMINARY: PRT; 27 AA.

AC Q51K66; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-DEC-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)] (Fragment).  
 GN POL.  
 DE Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 RN 111\_TaxID=11103;  
 RW 111\_TaxID=11103;  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=LB1;  
 RA Izopet J., Rostaing L., Sandres K., Cisterne J.M., Pasquier C.,  
 RA Rumeau J.L., Duffaut M., Durand D., Puel J.;  
 RT "Longitudinal analysis of Hepatitis C virus replication and liver  
 RT fibrosis progression in renal transplant recipients";  
 DE Hepatology 126:102-109 (2003).  
 DE ENBL:AP201348; AAP76599; The ENBL/GenBank/DBJ databases.  
 DR InterPro: IPR002531; HCV NS1.  
 DR Pfam: PF01560; HCV NS1.1.  
 DR KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON TER 1  
 FT NON TER 27  
 FT NON TER 27  
 SQ SEQUENCE 27 AA; 2768 MW; 2F457A89D77D2263 CRC64;  
 Query Match 100.0%; Score 20; DB 12; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 10 DRAT 13

RESULT 3  
 Q5X254 PRELIMINARY: PRT; 31 AA.

AC Q5X254; 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 3.6 kDa protein (Fragment).  
 OS Halobacterium salinarum (Halobacterium salinarum).  
 OC Archaea; Euryarchaeota; Halobacteriales;  
 OC Halobacteriaceae; Halobacter.  
 RN 111\_TaxID=2246;  
 RW 111\_TaxID=2246;  
 RC SEQUENCE FROM N.A.  
 RA Bidle K.A.;  
 RA "Differential expression of genes influenced by changing salinity  
 RT using RNA arbitrarily primed PCR in the archaeal halophile, Halobacter  
 RT salinarum";  
 RL Submitted (NOV-2001) to the ENBL/GenBank/DBJ databases.  
 DE ENBL:AF454092; AAL57845.1; --  
 DE Hypothetical protein.  
 FT NON TER 1  
 FT NON TER 31  
 SQ SEQUENCE 31 AA; 3609 MW; 682119A19273C9D0 CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 27 DRAT 30

RESULT 4

Q5UR68 PRELIMINARY: PRT; 45 AA.

AC Q5UR68; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Carboxypeptidase Y, Cpi (Fragment).  
 OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).  
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;  
 OC Mucor.  
 RN 111\_TaxID=4841;  
 RW 111\_TaxID=4841;  
 RC SEQUENCE  
 RC Strain=82105011; PubMed:1729337;  
 RA DiSanti M.E., Li O.H., Logan D.A.;  
 RA "Purification and characterization of a developmentally regulated  
 RT carboxypeptidase from Mucor racemosus";  
 RL J. Bacteriol. 174:447-455 (1992).  
 FT NON TER 1  
 FT NON TER 28  
 FT NON TER 45  
 FT NON TER 45  
 SQ SEQUENCE 45 AA; 5103 MW; A5F3B7471465465A CRC64;  
 Query Match 100.0%; Score 20; DB 3; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 16 DRAT 19

RESULT 5  
 Q5S604 PRELIMINARY: PRT; 46 AA.

AC Q5S604; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Sigma factor (Fragment).  
 GN FECl.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia coli.  
 RN 111\_TaxID=562;  
 RW 111\_TaxID=562;  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=95242013; PubMed=10227474;  
 RA Reingold J., Starr N., Maurer J., Lee M.D.;  
 RA "Identification of a new Escherichia coli She haemolysin homolog in  
 RT avian E. coli";  
 RL EMBO J. 16:125-134 (1999).  
 DE EMBL:AF052223; AAD28082.1; --  
 FT NON TER 46  
 FT NON TER 46  
 SQ SEQUENCE 46 AA; 5222 MW; 42D98F2A02EE4D19 CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 3 DRAT 6

RESULT 6  
 Q5XXT7 PRELIMINARY: PRT; 48 AA.

AC Q5XXT7; 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein RSC2026.





```

SQ SEQUENCE 64 AA; 7286 MW; 21256F1F01146535 CRC64;
Query Match 100.0%; Score 20; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRAT 4
DB 48 DRAT 51

RESULT 14
QSCFP1
ID QSCFP1 PRELIMINARY; PRT; 64 AA.
AC QSCFP1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Propaghe p13 protein 53.
DE PI353 OR IL1426.
GN PI353 OR IL1426.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN (1)
RW SEQUENCE FROM N.A.
RC STRAIN=IL1403.
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A.; Wincker P.; Manger S.; Jaillon O.; Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT *The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.*;
RL Genome Res. 11:731-753(2001).
RW (1)
KW Complete Proteome; AAA0524.1; -.
SQ SEQUENCE 54 AA; 7573 MW; 740DC4287228266F CRC64;
Query Match 100.0%; Score 20; DB 16; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRAT 4
DB 47 DRAT 50

RESULT 15
QNTNG
ID QNTNG PRELIMINARY; PRT; 66 AA.
AC QNTNG;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE BB94P8.1 (K1AA1326) (Fragment).
GN BB94P8.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RW SEQUENCE FROM N.A.
RC Wilson S.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL13274; CAB92740.1; -.
DR EMBL; AL13274; CAB92740.1; -.
FT NON-TER 66
SQ SEQUENCE 66 AA; 7022 MW; 218B52004B6B6A CRC64;
Query Match 100.0%; Score 20; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRAT 4

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DB 48 DRAT 51

Search completed: May 6, 2003, 15:02:48  
Job time : 16.2 secs

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Nucleic Acids Res. 22:4756-4767(1994).

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EMBL; M87049; -; NOT ANNOTATED CDS.  
EMBL; AE000457; -; NOT ANNOTATED CDS.  
EMBL; M66782; -; NOT ANNOTATED CDS.  
EMBL; AF005612; AAG59001.1; -;  
EMBL; AF005612; -; NOT ANNOTATED CDS.  
EMBL; AF025675; -; NOT ANNOTATED CDS.  
EMBL; AF025675; -; NOT ANNOTATED CDS.  
HYPOTHETICAL PROTEIN; Complete proteome.  
CONFLICT 60 67 DQPSOVNY -- MVHPR (IN REF. 2).  
SEQUENCE 67 AA; 7177 MW; 4452CF4BA555A/F9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
DB 55 DRAT 58

RESULT 2  
ENTRY NAME  
ID PYTH.TETH STANDARD; PRT; 70 AA.  
AC P43891.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)  
DE (UMP kinase) (Fragment).  
OS Thermus thermophilus  
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;  
OC Thermaceae; Thermus.  
OX NCBI\_TaxID=274;  
CC [1]  
CC SEQUENCE FROM N.A. 27634;  
CC KIRLIN-HS91649X ACC 27634;  
CC BLANK J. Neck S. Kreutzer R.  
CC "Elongation factor Ts from Thermus thermophilus -- overproduction in Escherichia coli, quaternary structure and interaction with elongation factor Tu.".  
CC Eur. J. Biochem. 236:222-227(1995).  
CC !- FUNCTION: URIDINE MONOPHOSPHATE KINASE (BY SIMILARITY).  
CC !- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.  
CC !- (BY SIMILARITY).  
CC !- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC !- SIMILARITY TO OTHER UMP KINASES; SOME, TO ASPARTOKINASES AND TO GLUTAMATE KINASES.

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EMBL; X83596; CA00589.1; -;  
EMBL; AF000048; Ad.kinase.  
EMBL; PF004049; Kinase; Pyrimidine biosynthesis.  
NON TER 70

SQ SEQUENCE 70 AA; 7629 MW; 7B8AB85DDA977CEB CRC64;

Query Match 100.0%; Score 20; DB 1; Length 70;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
DB 64 DRAT 67

RESULT 3  
ENTRY NAME  
ID YVAQ.VACC STANDARD; PRT; 77 AA.  
AC P05256.  
DT 01-SEP-1991 (Rel. 17, Created)  
DT 01-SEP-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 8.6 kDa protein.  
GN A ORF Q.  
OS Vaccinia virus (strain Copenhagen).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OC NCBI\_TaxID=10249;  
CN [1]  
CC [1]  
CC SEQUENCE FROM N.A.  
CC MEDLINE=91021037; PubMed=2219722;  
CC Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
CC Paolletti E.;  
CC "The complete DNA sequence of vaccinia virus."  
CC Virology 179:247-286(1990).  
CC COMPLETE GENOME.  
CC Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
CC Paolletti E.;  
CC "Appendix to 'The complete DNA sequence of vaccinia virus.'";  
CC Virology 179:537-563(1990).  
CC CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).

EMBL; X65227; A048178.1; -;  
EMBL; P05256; Po.vac.178.1; -;  
KW HYPOTHETICAL PROTEIN.  
SQ SEQUENCE 77 AA; 8635 MW; 12BBC61FF7472771 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
DB 23 DRAT 26

RESULT 4  
ENTRY NAME  
ID SCX7.TITRA STANDARD; PRT; 84 AA.  
AC P05256.  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Toxin gamma precursor.  
OS Tityus bahiensis (Brazilian scorpion).  
OC Arachnida; Metazoa; Arthropoda; Chelicerata; Scorpiones;  
OC Heterostomatida; Tityidae; Tityus.  
OX NCBI\_TaxID=50943;  
CN [1]

SQ SEQUENCE 84 AA; 9249 MW; 12B8C61FF7472771 CRC64;

RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-81.  
 RC MEDLINE=46107524; PubMed=6477555;  
 RX MEDLINE=46107524; PubMed=6477555;  
 RA Bittl C.R., Rochat H., Brando T., Martin M.-F.,  
 RA Calderon-Aranda E.S., Fletcher P.L. Jr., Martin B.M., Possani L.D.;  
 RT "Toxic peptides and genes encoding toxin gamma of the Brazilian  
 RT scorpions Tityus bahiensis and Tityus stigmurus";  
 RL Biochem. J. 313:753-760(1996).  
 CC -1- OF THE MAIN BINDING OF SODIUM CHANNELS AND INHIBITS THE INACTIVATION  
 CC -1- OF THE MAIN BINDING OF SODIUM CHANNELS AND INHIBITS THE INACTIVATION  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.  
 CC BETA-TOXIN SUBFAMILY.  
 CC HSSP; P01484; 1PTX.  
 CC Inter-Pro; IPR003614; Knc01.  
 DR Inter-Pro; IPR002061; Scorpion\_toxinL.  
 DR Pfam; PF00537; toxin\_3; 1.  
 DR SMART; SM00505; Knc01; 1.  
 DR SMART; SM00505; Knc01; 1.  
 KW Neurotoxin; Sodium channel inhibitor; Amidation; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 81 TOXIN GAMMA.  
 FT DISULFID 31 81 BY SIMILARITY.  
 FT DISULFID 35 57 BY SIMILARITY.  
 FT DISULFID 43 62 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT MO\_RES 81 81 AMIDATION (G-82 PROVIDE AMIDE GROUP)  
 FT MO\_RES 81 81 (PROBABLE)  
 SQ SEQUENCE 84 AA; 9384 MW; A24A2ACATF768136 CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78  
 RESULT 5  
 AC SCV7\_TJSE STANDARD; PRT; 84 AA.  
 AC P15226;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Toxin VII precursor (TetX-VII) (Tityustoxin VII) (Ts VII) (Toxin  
 DE II-11) (Toxin III-10) (Toxin gamma) (Toxin T2-IV).  
 DE Tityus serrulatus (Brazilian scorpion).  
 OC Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Buthoidea; Buthidae; Tityus.  
 ON NCBI\_TaxID=6887;  
 RX SEQUENCE FROM N.A.  
 RC TISSUE=Venom;  
 RX MEDLINE=92296001; PubMed=1339357;  
 RA Martin-Bacaire M.-F., Ceard B., Ribeiro A.M., Diniz C.R., Rochat H.,  
 RA "Molecular cloning and nucleotide sequence analysis of a cDNA  
 RT encoding the main beta-neurotoxin from the venom of the South  
 RT American scorpion Tityus serrulatus";  
 RL FEBS Lett. 302:220-222(1992).  
 CC (2)  
 CC SEQUENCE FROM N.A.  
 RC TISSUE=Venom; PubMed=824366;  
 RX MEDLINE=824366; PubMed=824366;  
 RA Becerril B., Corona M., Mejia M.C., Martin B.M., Bolivar P.,  
 RA Possani L.D.;  
 RT "The genomic region encoding toxin gamma from the scorpion Tityus  
 RT serrulatus contains an intron";  
 RL FEBS Lett. 335:6-8(1993).  
 CC (3)  
 CC SEQUENCE OF 21-81.

RC TISSUE=Venom;  
 RX MEDLINE=46107524; PubMed=6477555;  
 RX MEDLINE=46107524; PubMed=6477555;  
 RA Bittl C.R., Rochat H., Brando T., Martin M.-F.,  
 RA Calderon-Aranda E.S., Fletcher P.L. Jr., Martin B.M., Possani L.D.;  
 RT "Amino acid sequence of toxin VII, a beta-toxin from the venom of the  
 RT scorpion Tityus serrulatus";  
 RL Biochem. Biophys. Res. Commun. 122:1146-1153(1984).  
 CC (4)  
 CC SEQUENCE OF 21-81.  
 CC MEDLINE=91311623; PubMed=1991690;  
 RA Possani L.D., Martin B.M., Fletcher P.L. Jr.;  
 RT "Discharge effect on pancreatic exocrine secretion produced by toxins  
 RT purified from Tityus serrulatus scorpion venom";  
 RL J. Biol. Chem. 266:3178-3185(1991).  
 CC (5)  
 CC SEQUENCE OF 21-82.  
 CC MEDLINE=91311623; PubMed=1991690;  
 RA Possani L.D., Martin B.M., Mochica-Morales J., Svendsen I.;  
 RT "Purification and chemical characterization of the major toxins from  
 RT the venom of the Brazilian scorpion Tityus serrulatus Lutz and Mello";  
 RL Carlsberg Res. Commun. 46:195-205(1981).  
 CC (6)  
 CC SEQUENCE OF 21-46.  
 CC TISSUE=Venom;  
 RC MEDLINE=9203285; PubMed=1926167;  
 RX MEDLINE=9203285; PubMed=1926167;  
 RA Giglio J.R.; Arantes E.C.; Prado W.A., Riccioppo Neto F.,  
 RA "Further characterization of toxins TIV (TetX-III) and T2IV from  
 RT Tityus serrulatus scorpion venom";  
 RL Toxicon 29:663-672(1991).  
 CC -1- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION  
 CC OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.  
 CC BETA-TOXIN SUBFAMILY.  
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 CC modified and this statement is not removed" added. If you are a commercial  
 CC entity, you must also send an email to license@sib.ch or send an email to  
 CC or send an email to license@sib.ch.  
 CC EMBL; X66256; CAA69802.1; -;  
 CC EMBL; X66256; CAA69802.1; -;  
 CC PIR; A39510; A39510.  
 CC PIR; A39510; A39510.  
 CC PIR; S39438; S39438.  
 CC HSSP; P01484; 1PTX.  
 DR Inter-Pro; IPR003614; Knc01.  
 DR Inter-Pro; IPR002061; Scorpion\_toxinL.  
 DR Pfam; PF00537; toxin\_3; 1.  
 DR SMART; SM00505; Knc01; 1.  
 DR SMART; SM00505; Knc01; 1.  
 DR TISSUE=Venom; Sodium channel inhibitor; Amidation; Signal.  
 FT CHAIN 21 81 TOXIN VII.  
 FT DISULFID 31 81 BY SIMILARITY.  
 FT DISULFID 35 57 BY SIMILARITY.  
 FT DISULFID 43 62 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT MO\_RES 81 81 AMIDATION (G-82 PROVIDE AMIDE GROUP).  
 FT MO\_RES 84 AA; 9384 MW; 430F3CAV4823E77 CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78



Best Local Similarity 100.0%; Pred. No. 68;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
DB 18 DRAT 21

## RESULT 8

Y44D SCHPO STANDARD; PRT; 91 AA.  
ID C09730 CHUPO  
AC 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein C31A2.13c in chromosome 1.  
DN SPAC31A2.13c.  
GN Schizosaccharomyces pombe (Fission yeast)  
OC Schizosaccharomycetes; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes;  
CC NCBI\_TaxID=4896;  
CC (1)  
RN SEQUENCE FROM N.A.  
RP STRAIN=972;  
RC MEDLINE=21849401; PubMed=1899360;  
RA Gwladys, A., Lynne M., Lynne R., Stewart A.,  
RA Spouras J., Peat N., Hayler J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
RA Holroyd S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp J.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,  
RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritsc C., Holzer E., Moestl D., Hilbert H.,  
RA Borczyk K., Langston W., Beckler H., Hubert R., Kinsdel, B., Kohl T.M.,  
RA Goffeau A., Cadieu W., Dreano S., Gloux S., Lelaure V., Mortier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Dominguez A., Revuelta J.L., Moreno S., Sanchez M., del Rey F., Benito J.,  
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Spakowaki G.V., Ussery D., Barrett B.G., Nurse P.,  
RA Nature 415:871-880 (2002)  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL; Z50113; CAA90471.1; .  
DR TRANSMEM 68 84 POTENTIAL.  
SQ SEQUENCE 91 AA; 10542 MW; 78F6695CEB816CBB CMC64;

Query March 100.0%; Score 20; DB 1; Length 91;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
DB 37 DRAT 40

## RESULT 9

Y44D MYCTU STANDARD; PRT; 104 AA.  
ID UR52 MYCTU  
AC P50018;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urease beta subunit, Ec 3.5.1.5 (urea amidohydrolase).  
DN Schizosaccharomyces pombe (Fission yeast)  
GN Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteriales; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
CC NCBI\_TaxID=1773;  
CC (1)  
RN SEQUENCE FROM N.A.  
RP STRAIN=972;  
RC MEDLINE=96004620; PubMed=7568014;  
RA Ruyat J.M., Berthet F.X., Gicquel B.,  
RT "The urease locus of Mycobacterium tuberculosis and its utilization  
RT for the demonstration of allelic exchange in Mycobacterium bovis  
RT bacillus Calmette-Guerin.";  
RT Proc. Natl. Acad. Sci. U.S.A. 92:8760-8772 (1995).  
RN (2)  
RN SEQUENCE FROM N.A.  
RP STRAIN=972;  
RC MEDLINE=96032403; PubMed=7559354;  
RA Clemens D.L., Lee B.Y., Horwitz M.A.,  
RT "Purification, characterization, and genetic analysis of  
RT Mycobacterium tuberculosis urease, a potentially critical determinant  
RT of host-pathogen interaction.";  
RL J. Bacteriol. 177:5644-5652 (1995).  
RN (3)  
RN SEQUENCE FROM N.A.  
RP STRAIN=H37Rv;  
RC MEDLINE=9825987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekala F.,  
RA Badoock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Oliver S., O'Garra J., Quail M.A., Rastam M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.,  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence.";  
RL Nature 393:537-544 (1998).  
RN (4)  
RN SEQUENCE FROM N.A.  
RP STRAIN=CDC 1551; Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., DeBoy R., Dodson R., Gwim M.L., Haft D., Hickey E.,  
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Ueberall T., Weidman J., Khouri H., Gill J., Milka A.,  
RA Bishai W.,  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Urea + H(2O) = CO(2) + 2 NH(3).  
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHER UREASES BETA SUBUNIT.  
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CC  
CC EMBL; L41141; AAC37006.1; .  
DR EMBL; U33011; AAC43474.1; .

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DR EMBL: Z62859; CAB06138.1; -
DR ENR: A24677; F0446168.1; -
DR HSP: P18315; 1; IMB.
DR TIGR: M1897; -
DR Tuberculin; Rv1849; -
DR InterPro: IPR002019; Urease_beta.
DR Pfam: PF00699; Urease_beta; 1.
DR ProDom: PD003236; Urease_beta; 1.
DR TIGRfam: TIGR00192; urease_beta; 1.
DR KX: Q9JW46; Urease proteome.
DR KX: Q9JW46; Urease proteome.
SQ SEQUENCE 104 AA; 1150 MW; D62ICE33M7304EO CRC64;
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 104;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DRAT 4
DB 53 DRAT 56
RESULT 10
VSTM_NPVP
ID VSTM_NPVP STANDARD; PRT; 109 AA.
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE ECORI-T site protein ETM homolog.
CC ETM.
OS Orygia pseudotaugeta multicapsid polyhedrosis virus (OpMPV).
CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
CC Orygia pseudotaugeta multicapsid polyhedrosis virus.
CC NCBI_TaxID=164623;
RN NCBI:164623;
RX MEDLINE=97271300; PubMed=9126251;
RP SEQUENCE FROM N.A.
RA Ahrens C.H.; Russell R.R.; Funk C.J.; Evans J.; Harwood S.;
RA Rohmann G.F.;
RT polyhedrosis virus;
RL Virology 229:381-399 (1997).
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CC or send an email to license@ebi.ac.uk).
DR EMBL: U75930; AAC59051.1; -
DR KX: Q9JW46; Urease proteome.
DR KX: Q9JW46; Urease proteome.
SQ SEQUENCE 109 AA; 12053 MW; 597B7F7137389454 CRC64;
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 109;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DRAT 4
DB 33 DRAT 36
RESULT 11
RNPA_NEIMA
ID RNPA_NEIMA STANDARD; PRT; 121 AA.
AC Q9JW46;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
DE P protein) (Protein C5).
OS Neisseria meningitidis (serogroup B).
CC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
CC NCBI_TaxID=491;
RN NCBI:491;
RP SEQUENCE FROM N.A.
RA STRAIN=MC58 / Serogroup B;
RT meningitidis 22491;
RL Nature 404:502-506 (2000).
CC -1- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5'-terminus. It can also
CC cleave other RNA substrates such as 4.5S RNA. The protein
CC component plays an auxiliary but essential role in vivo by binding
CC to the ribosome (by similarity), promoting the substrate specificity
CC of the ribosome (by similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.
CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (by similarity).
CC -1- SIMILARITY: BELONGS TO THE RNPA FAMILY.
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CC or send an email to license@ebi.ac.uk).
DR EMBL: AL162753; CAB83843.1; -
DR InterPro: IPR000100; Ribonuclease_P.
DR Pfam: PF00825; Ribonuclease_P; 1.
DR ProDom: PD003629; Ribonuclease_P; 1.
DR TIGRfam: TIGR00188; rnpA; 1.
DR KX: Q9JW46; Urease proteome.
DR KX: Q9JW46; Urease proteome.
SQ SEQUENCE 121 AA; 14268 MW; 860703F3365E0F2 CRC64;
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 121;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DRAT 4
DB 94 DRAT 97
RESULT 12
RNPA_NEIMA
ID RNPA_NEIMA STANDARD; PRT; 121 AA.
AC Q9JW46;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
DE P protein) (Protein C5).
OS Neisseria meningitidis (serogroup B).
CC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
CC NCBI_TaxID=491;
RN NCBI:491;
RP SEQUENCE FROM N.A.
RA STRAIN=MC58 / Serogroup B;
RT meningitidis 22491;
RL Nature 404:502-506 (2000).
CC -1- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5'-terminus. It can also
CC cleave other RNA substrates such as 4.5S RNA. The protein
CC component plays an auxiliary but essential role in vivo by binding
CC to the ribosome (by similarity), promoting the substrate specificity
CC of the ribosome (by similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.
CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (by similarity).
CC -1- SIMILARITY: BELONGS TO THE RNPA FAMILY.
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CC or send an email to license@ebi.ac.uk).
DR EMBL: AL162753; CAB83843.1; -
DR InterPro: IPR000100; Ribonuclease_P.
DR Pfam: PF00825; Ribonuclease_P; 1.
DR ProDom: PD003629; Ribonuclease_P; 1.
DR TIGRfam: TIGR00188; rnpA; 1.
DR KX: Q9JW46; Urease proteome.
DR KX: Q9JW46; Urease proteome.
SQ SEQUENCE 121 AA; 14268 MW; 860703F3365E0F2 CRC64;
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 121;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DRAT 4
DB 94 DRAT 97

```



Wed May 7 14:15:08 2003

us-09-851-422b-2.rsp

Query Match 100.0%; Score 20; DB 1; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 111 DRAT 114

DB 48 DRAT 51

Search completed: May 6, 2003, 15:01:29  
 Job time : 6 secs

RESULT 15  
 ADF1\_MAIZE STANDARD; PRT; 139 AA.  
 AD Q176  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Actin-depolymerizing factor 3 (ADP 3) (ZmADF3) (ZmADF3).  
 GN ADF3 OR ADP3.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Eudicotyledons; Gunnerales; Zingiberales; Zingiberaceae; Zingiber  
 OC Panicoidae; Andropogoneae; Zea.  
 OC NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Leaf;  
 RX MEDLINE=96293540; PubMed=8693008;  
 RA Hogeney P, Anthony R.G., Maciver S.K., Jiang C.J., Khan S., Weeds A.G.,  
 RA "pollen specific expression of maize genes encoding actin  
 RT depolymerizing factor-like proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7415-7420(1996).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE=96079240; PubMed=9418045;  
 RA Hogeney P, Anthony R.G., Maciver S.K., Jiang C.J., Khan S., Weeds A.G.,  
 RT "The maize actin-depolymerizing factor, ZmADF3, redistributes to the  
 RT growing tip of elongating root hairs and can be induced to  
 RT translocate into the nucleus with actin.";  
 RL Plant J. 12:1035-1043(1997).  
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS  
 CC (IF-ACTIN) AND BINDS TO ACTIN MONOMERS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Has root hairs emergence and the  
 CC actin-depolymerizing factor-like proteins. The actin-depolymerizing factor  
 CC at the tip of the emerging hair and remains in this position as  
 CC elongation proceeds.  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues except pollen.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
 CC  
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 CC -----  
 CC EMBL; X97726; CMA6311.1; -;  
 CC EMBL; X97726; CMA6311.1; -;  
 CC InterPro; IPR002108; Actbind\_cofin.  
 CC Pfam; PF00241; cofilin\_ADF\_1.  
 CC ProDom; PD002129; Actbind\_cofin; 1..  
 CC SMART; SM00102; ADF; 1.  
 CC PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 CC Actin-binding; Multigene family.  
 CC PIRANKA; PIRANKA; ACTIN-BINDING (POTENTIAL).  
 CC SEQUENCE 139 AA; 15900 MW; 28FC8C518022C87 CRC64;  
 CC

Query Match 100.0%; Score 20; DB 1; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 1e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4



GenCore version 5.1.4\_p5\_4576  
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OM protein - protein search, using sw model

Run on: May 6, 2003, 14:59:05 ; Search time 7 seconds  
(without alignments)  
54,934 Million cell updates/sec

Title: US-09-851-422B-2

Perfect score: 20

Sequence: 1 DRAT 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 08

Maximum March 1008

Listing first 45 summaries

Database : PIR-73.\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	20	100.0	28	2	A44923
2	20	100.0	63	2	F84284
3	20	100.0	64	2	F81950
4	20	100.0	64	2	B86803
5	20	100.0	67	2	B86806
6	20	100.0	67	2	B86807
7	20	100.0	70	2	S51096
8	20	100.0	70	2	A60912
9	20	100.0	77	2	D42525
10	20	100.0	84	2	S62867
11	20	100.0	84	2	S62868
12	20	100.0	84	2	S21158
13	20	100.0	91	2	S55697
14	20	100.0	91	2	C83804
15	20	100.0	91	2	A70665
16	20	100.0	104	2	QJ1240
17	20	100.0	105	2	QJ1823
18	20	100.0	105	2	T10321
19	20	100.0	109	2	T10321
20	20	100.0	111	2	AC2497
21	20	100.0	111	2	T13298
22	20	100.0	113	2	T13298
23	20	100.0	115	2	S68316
24	20	100.0	118	2	E30540
25	20	100.0	118	2	H97644
26	20	100.0	119	2	T11049
27	20	100.0	120	2	I39623
28	20	100.0	121	2	F81973
29	20	100.0	121	2	H81027

30 20 100.0 122 2 AH2170  
31 20 100.0 123 2 T07886  
32 20 100.0 123 2 C83148  
33 20 100.0 129 2 C83148  
34 20 100.0 130 2 E87024  
35 20 100.0 135 2 C82438  
36 20 100.0 138 2 F81243  
37 20 100.0 138 2 G82015  
38 20 100.0 139 2 T02914  
39 20 100.0 141 2 S72386  
40 20 100.0 142 2 T02914  
41 20 100.0 144 2 E72647  
42 20 100.0 144 2 T01476  
43 20 100.0 145 2 A64046  
44 20 100.0 145 2 C82513  
45 20 100.0 151 2 C84953

ferredoxin [import  
protein kinase (EC  
3.6.1.34)  
high molecular weight  
probable membrane  
regulator of nucle  
DnaK suppressor pr  
probable DnaK supp  
actin-depolymerizi  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
dosage-dependent d  
conserved hypothet  
dnaK suppressor pr

#### ALIGNMENTS

##### RESULT 1

A44923

carboxypeptidase 3 - Rhizomucor circinelloides f. lusitanicus (fragment)

C:Species: Rhizomucor circinelloides f. lusitanicus

C:Update: 1-Apr-1993 Sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994

A:Accession: A44923

R:Disanto, M.E.; Li, Q.H.; Logan, D.A.

J. Bacteriol. 174, 447-455, 1992

A:Title: Purification and characterization of a developmentally regulated carboxypeptid

A:Reference number: A44923; PMID:92105011; PMID:1729237

A:Accession: A44923

A:Status: preliminary

A:Molecule type: Protein

A:Note: Sequence extracted from NCBI backbone (NCBIP:75614)

Query Match 100.0%; Score 20; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

DB 16 DRAT 19

##### RESULT 2

F84284

hypothetical protein Vmg1295h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Update: 02-Feb-2001 Sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

A:Accession: F84284

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl,

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, G.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lasky,

A:Update: 02-Feb-2001 Sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

A:Reference number: A84160; PMID:20504483; PMID:1101950

A:Accession: F84284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-63 <STO>

A:Cross-references: GB:A8004437; NID:g10580814; FIDN:AAG19642.1; GSPDB:GN00138

C:Genetic:

A:Gene: Vmg1295h

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 63;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

DB 16 DRAT 19

Db 30 DRAT 33

## RESULT 3

Biochemical protein - Rhizobium leguminosarum (fragment)

C:Species: Rhizobium leguminosarum

C&gt;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 21-Jul-2000

C/Accession: S11950

R/Colonna-Romano, S.; Arnold, W.; Schluter, A.; Bolstad, P.; Puchler, A.; Priefer, U.H.

Mol. Gen. Genet. 223, 138-147, 1990

A&gt;Title: An Etn-like protein encoded in Rhizobium leguminosarum biovar viciae shows str

A/Accession: S11950

A/Reference number: A85480; MUID:91060854; PMID:2175385

A/Molecule type: DNA

A/Residues: 1-64 &lt;COL&gt;

A/Cross-references: EMBL:X55788; NID:g111223; PIDN:CAA39311.1; PID:g3980213

C:Superfamily: acyl carrier protein; acyl carrier protein homology

C:Keywords: carrier protein

F:13-64/domain: acyl carrier protein homology (fragment) &lt;ACP&gt;

Query Match 100.0%; Score 20; DB 2; Length 64;

Best Local Similarity 100.0%; Pred. No. 1.e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

Db 32 DRAT 35

## RESULT 4

prophage p13 protein 53 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C&gt;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

R/Bolotin-A. M. Mauger, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A&gt;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A/Reference number: A86625; MUID:21235186; PMID:11337471

A/Accession: B86803

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-570

A/Cross-references: GB:AF005176; PID:g12724415; PIDN:AAK05524.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: p1353

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 64;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

Db 47 DRAT 50

## RESULT 5

hypothetical protein Z5325 [imported] - Escherichia coli (strain O157:H7, substrain EDL5

C:Species: Escherichia coli

C&gt;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.G.; Grobeck, S.J.; Davis, N.W.; Lin, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

A&gt;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: B86067

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-67 &lt;STO&gt;

A/Cross-references: GB:AB005174; NID:g12518676; PIDN:AAG59001.1; GSPDB:GN00145; UWGP:Z5325  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z5325

Query Match 100.0%; Score 20; DB 2; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

Db 55 DRAT 58

## RESULT 6

probable lipoprotein yifL [imported] - Salmonella enterica subsp. enterica serovar Typhi

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A&gt;Note: this species has also been called Salmonella typhi

C&gt;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

A/Accession: A00919

R/Bowman, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

Ch.T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moutle, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Authors: Barry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A&gt;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A/Reference number: A00919

A/Accession: A00919

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-67 &lt;PAR&gt;

A/Cross-references: GB:AL513382; PIDN:CAD09374.1; PID:g16504492; GSPDB:GN00176

C:Genetics:

A:Gene: yifL

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 67;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

Db 55 DRAT 58

## RESULT 7

UMP kinase - Thermus aquaticus (fragment)

C:Species: Thermus aquaticus

C&gt;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 24-Sep-1999

R/Blank, J.; Grillmeyer, N.; Kreutzer, R.; Srdinzi, M.

A/Accession: S51096

A/Reference number: S51096

A/Accession: S51096

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-70 &lt;BLA&gt;

A/Cross-references: GB:U019359; NID:g619569; PIDN:CAA58579.1; PID:g619571

A&gt;Note: the source is designated as Thermus thermophilus

C:Superfamily: uridine 5'-monophosphate kinase

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 70;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4

Db 64 DRAT 67

## RESULT 8

A60912  
 C:Species: Gallus gallus (chicken)  
 C:Accession: G81193  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 12-Sep-1997  
 R:McDonnell, D.P.; Mangelsdorf, D.J.; Pike, J.W.; Hausaler, M.R.; O'Malley, B.W.  
 Science 235, 1214-1217, 1987  
 A>Title: Molecular cloning of complementary DNA encoding the avian receptor for vitamin A  
 A:Reference number: A60912; MUID:87149040; PMID:3029866  
 A:Species: Gallus gallus (chicken)  
 A:Accession: G81193  
 A:Molecule type: mRNA  
 A:Keywords: vitamin A; retinoic acid sequence not shown; not compared with conceptual translation  
 A:Residues: 1-70 <NC>  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C:Keywords: DNA binding; zinc finger  
 F:1-70/Domain: erba transforming protein homology (fragment) <ERBA>  
 Query Match 100.0%; Score 20; DB 2; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 1 DRAT 4  
 DB 8 DRAT 11  
 RESULT 9  
 D42525  
 A:ORF-Q protein - vaccinia virus (strain Copenhagen)  
 C:Species: vaccinia virus  
 A:Note: host Homo sapiens (man)  
 C>Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 08-Apr-1994  
 C:Accession: D42525  
 A:Reference number: A33172  
 A:Accession: D42525  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-77 <QJ>

Query Match 100.0%; Score 20; DB 2; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 1 DRAT 4  
 DB 23 DRAT 26  
 RESULT 10  
 D62867  
 toxin gamma precursor - Tityus stigmurus  
 C:Species: Tityus stigmurus  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
 R:Beccerilli, B.; Corona, M.; Coronas, F.I.V.; Zamudio, F.; Calderon-Aranda, E.S.; Fletcher  
 Biochem. J. 313, 753-760, 1996  
 A>Title: Toxic peptides and genes encoding toxin gamma of the Brazilian scorpions Tityus  
 A:Reference number: S62861; MUID:96190713; PMID:8611151  
 A:Accession: S62867  
 A:Molecule type: DNA  
 A:Residues: 1-84 <BEC>  
 A:Accession: S62865  
 A:Residues: 1-84 <BEC>  
 A:Molecule type: protein  
 C:Superfamily: scorpion neurotoxin  
 C:Keywords: amidated carboxyl end; neurotoxin; venom  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-82/Product: toxin gamma #status predicted <MAT>  
 F:31-81.35-57.43-62.47-64/Dsulfide bonds: #status predicted  
 F:81/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly

Query Match 100.0%; Score 20; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78  
 RESULT 11  
 D62867  
 toxin gamma precursor - Tityus bahiensis  
 C:Species: Tityus bahiensis  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
 R:Beccerilli, B.; Corona, M.; Coronas, F.I.V.; Zamudio, F.; Calderon-Aranda, E.S.; Fletcher  
 Biochem. J. 313, 753-760, 1996  
 A>Title: Toxic peptides and genes encoding toxin gamma of the Brazilian scorpions Tityus  
 A:Reference number: S62861; MUID:96190713; PMID:8611151  
 A:Accession: S62868  
 A:Molecule type: DNA  
 A:Residues: 1-84 <BEC>  
 A:Accession: S62861  
 A:Molecule type: protein  
 A:Residues: 21-81 <BEW>  
 C:Superfamily: scorpion neurotoxin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-82/Product: toxin gamma #status experimental <MAT>  
 F:31-81.35-57.43-62.47-64/Dsulfide bonds: #status predicted  
 F:81/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly  
 Query Match 100.0%; Score 20; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78  
 RESULT 12  
 S21158  
 neurotoxin TeVII precursor - Brazilian scorpion  
 N:Alternate names: beta-neurotoxin; neurotoxin II-11; neurotoxin III-10; toxin gamma  
 C:Species: Tityus serrulatus (Brazilian scorpion)  
 C>Date: 22-Nov-1993 #sequence\_revision 04-Oct-1996 #text\_change 16-Jul-1999  
 C:Accession: S21158; S39438; A39510; S32790  
 R:Martin-Eaucalaire, M.F.; Ceard, B.; Ribeiro, A.M.; Diniz, C.R.; Rochat, H.; Bougis, P.  
 FEBS Lett 302, 220-222, 1994  
 A>Title: The amino acid and nucleotide sequence analysis of a cDNA encoding the main  
 A:Reference number: S21158; MUID:92290001; PMID:1339357  
 A:Accession: S21158  
 A:Molecule type: mRNA  
 A:Residues: 1-84 <MAR>  
 A:Cross-references: EMBL:X66256; NID:G312021; PIDN:CAAM6982.1; PID:G312022  
 R:Beccerilli, B.; Corona, M.; Mejia, M.C.; Martin, B.M.; Lucas, S.; Bolivar, F.; Possani,  
 A:Title: The amino acid sequence of the toxin gamma from the scorpion Tityus serrulatus  
 A:Reference number: S39438; MUID:94063080; PMID:8243566  
 A:Accession: S39438  
 A:Molecule type: DNA  
 A:Residues: 1-84 <BEC>  
 A:Cross-references: EMBL:X66941; NID:G453105; PIDN:AAB29128.1; PID:G453106  
 R:Possani, L.D.; Martin, B.M.; Fletcher, M.D.; Fletcher Jr., P.B.  
 A:Title: Discharge effect on pancreatic exocrine secretion produced by toxins purified  
 A:Reference number: A39510; MUID:91331623; PMID:1993690  
 A:Accession: A39510  
 A:Molecule type: protein  
 A:Residues: 21-81 <POS>  
 R:Possani, L.D.; Martin, B.M.; Svendsen, I.; Rode, G.S.; Erickson, B.W.  
 Biochem. J. 229, 739-750, 1985

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submitted to the EMBL Data Library, July 1995
A:Reference number: Z21731
A:Accession: T38611
A:Status: preliminary; translated from GS/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-91 <DE2>
A:Cross-references: EMBL:Z50113; NID:g914878; PIDN:CM90471.1; PID:g914891; GSPDB:GN000.
C:Experimental source: strain 972H; cosmid c31a2
A:Gene: SPAC31A2.13c
A:Map position: 1
A:Introns: 39/3

Query Match      100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRAT 4
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Db 37 DRAT 40

RESULT 15
Biochemical protein BH1235 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
A:Accession: C83804
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, P.; Hirai,
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; WUID:20512582; PMID:11058132
A:Gene: BH1235
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04954.1; GSPDB:GN000.
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1235

Query Match      100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRAT 4
    |||||
Db 31 DRAT 34

Search completed: May 6, 2003, 15:03:29
Job time : 9 secs
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Result	No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	19	9	US-10-067-813-5			Sequence 5, Appli
2	20	100.0	26	9	US-10-043-487-532			Sequence 532, App
3	20	100.0	25	9	US-10-142-231-37			Sequence 37, Appl
4	20	100.0	57	10	US-09-864-761-37634			Sequence 37634, A
5	20	100.0	66	10	US-09-864-761-35163			Sequence 36163, A
6	20	100.0	77	10	US-10-128-806-801962			Sequence 80796, App
7	20	100.0	72	10	US-09-864-761-37634			Sequence 37634, A
8	20	100.0	78	10	US-09-864-761-34713			Sequence 34713, A
9	20	100.0	84	10	US-10-092-154-620			Sequence 620, App
10	20	100.0	84	10	US-09-764-847-620			Sequence 620, App
11	20	100.0	86	9	US-09-992-598-274			Sequence 274, App
12	20	100.0	86	9	US-09-989-293A-274			Sequence 274, App
13	20	100.0	86	9	US-09-989-735-274			Sequence 274, App
14	20	100.0	86	9	US-09-990-444-274			Sequence 274, App
15	20	100.0	86	9	US-09-969-730-274			Sequence 274, App
16	20	100.0	86	9	US-09-991-181-274			Sequence 274, App
17	20	100.0	86	9	US-09-931-687-274			Sequence 274, App
18	20	100.0	86	9	US-09-993-687-274			Sequence 274, App
19	20	100.0	86	9	US-09-989-734-274			Sequence 274, App

; TITLE OF INVENTION: PRO

FILE OF INVENTION: mammalian polypeptides

FILE REFERENCE: B4778A  
 CURRENT APPLICATION NUMBER: US/10/043,487  
 PRIOR FILING DATE: 2002-04-30  
 PRIOR FILING DATE: 2002-04-30  
 PRIOR FILING DATE: 2002-04-30  
 NUMBER OF SEQ ID NOS: 561  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 532  
 LENGTH: 26  
 TYPE: PRT  
 ORGANISM: Shigella flexneri  
 US-10-043-487-532

Query Match 100.0%; Score 20; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4

Db 11 DRAT 14

RESULT 3

US-10-142-231-37

Sequence 37, Application US/10142231

Publication No. US2003007796A1

GENERAL INFORMATION: Rodney et al.

FILE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES

FILE REFERENCE: 62773

CURRENT APPLICATION NUMBER: US/10/142,231

PRIOR FILING DATE: 2002-05-08

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 37

LENGTH: 50

TYPE: PRT

ORGANISM: Taxus cuspidata

US-10-142-231-37

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 50;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4

Db 26 DRAT 29

RESULT 4

US-09-864-761-37634

Sequence 37634, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenhang

FILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

SEQUENCE ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 1017  
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 37634  
 LENGTH: 57  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: INFORMATION: MAP TO M132722.1  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.7  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.1  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7  
 OTHER INFORMATION: EXPRESSED IN HUMAN TESTIS, SIGNAL = 2.6  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2  
 OTHER INFORMATION: EXPRESSED IN HELA00, SIGNAL = 3  
 OTHER INFORMATION: SWISSPROT HIT: P41235, EVALUATE 3.00e-30  
 OTHER INFORMATION: EST\_HUMAN HIT: AUI30255.1, EVALUATE 6.00e-13  
 US-09-864-761-37634

Query Match 100.0%; Score 20; DB 10; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4

Db 26 DRAT 29

RESULT 5

US-09-864-761-36163

Sequence 36163, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenhang

FILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

SEQUENCE ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2001-05-23



1 PRIOR FILING DATE: 2000-02-04  
 2 PRIOR APPLICATION NUMBER: US 60/207,456  
 3 PRIOR FILING DATE: 2000-05-26  
 4 PRIOR APPLICATION NUMBER: US 09/632,366  
 5 PRIOR FILING DATE: 2000-08-03  
 6 PRIOR APPLICATION NUMBER: US 09/632,366  
 7 PRIOR FILING DATE: 2000-10-04  
 8 PRIOR APPLICATION NUMBER: US 60/236,359  
 9 PRIOR FILING DATE: 2000-09-27  
 10 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 11 PRIOR FILING DATE: 2001-01-30  
 12 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 13 PRIOR FILING DATE: 2001-01-30  
 14 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 15 PRIOR FILING DATE: 2001-01-30  
 16 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 17 PRIOR FILING DATE: 2001-01-30  
 18 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 19 PRIOR FILING DATE: 2001-01-30  
 20 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 21 PRIOR FILING DATE: 2001-01-30  
 22 PRIOR APPLICATION NUMBER: PCT/US01/00663  
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 24 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 25 PRIOR FILING DATE: 2001-01-30  
 26 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 27 PRIOR FILING DATE: 2001-01-30  
 28 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 29 PRIOR FILING DATE: 2000-09-21  
 30 PRIOR APPLICATION NUMBER: US 60/234,687  
 31 PRIOR FILING DATE: 2000-09-21  
 32 PRIOR APPLICATION NUMBER: US 09/608,408  
 33 PRIOR FILING DATE: 2000-06-30  
 34 PRIOR APPLICATION NUMBER: US 09/774,203  
 35 PRIOR FILING DATE: 2001-01-29  
 36 NUMBER OF SEQ ID NOS: 49117-55  
 37 SEQ ID NO 34962  
 38 LENGTH: 72  
 39 TYPE: PRT  
 40 ORGANISM: Homo sapiens  
 41 FEATURE:  
 42 OTHER INFORMATION: MAP TO ALL21755.1 SIGNAL = 1.8  
 43 OTHER INFORMATION: EXPRESSED IN BONE MARROW SIGNAL = 2  
 44 OTHER INFORMATION: EXPRESSED IN LUNG SIGNAL = 1.3  
 45 OTHER INFORMATION: EXPRESSED IN BRAIN SIGNAL = 1.8  
 46 OTHER INFORMATION: EXPRESSED IN BT474 SIGNAL = 1.4  
 47 OTHER INFORMATION: EXPRESSED IN PLACENTA SIGNAL = 2.7  
 48 OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 2.3  
 49 OTHER INFORMATION: EXPRESSED IN HELI00 SIGNAL = 1.9  
 50 OTHER INFORMATION: EXPRESSED IN HONE MARROW SIGNAL = 3.1  
 51 OTHER INFORMATION: EXPRESSED IN FETAL LIVER SIGNAL = 1.6  
 52 OTHER INFORMATION: EST HUMAN HIT: AM99712.1 EVALUATE 2.00e-25  
 53 OTHER INFORMATION: SWISSPROT HIT: P08547, EVALUATE 6.00e-21  
 54 US-09-864-761-34962

Query Match 100.04; Score 20; DB 10; Length 72;  
 Best Local Similarity 100.04; PctId 100.04; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DRAT 4  
 Db 52 DRAT 55

RESULT 8  
 US-09-864-761-34713  
 1 Sequence 34713, Application US/09864761  
 2 Patent No. US2002048763A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Penn, Sharron G.  
 5 APPLICANT: Rank, David R.

1 APPLICANT: Hanzel, David K.  
 2 APPLICANT: Chen, Wensheng  
 3 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 4 THE REFERENCE: PCT/US01/00666  
 5 CITE REFERENCE: PCT/US01/00666  
 6 CITE REFERENCE: PCT/US01/00666  
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Query Match 100.04; Score 20; DB 10; Length 78;  
 Best Local Similarity 100.04; PctId 100.04; Indels 0; Gaps 0;  
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Qy 1 DRAT 4  
 Db 58 DRAT 61



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RESULT 9
US-09-154-620
Sequence 620, Application US/10092154
GENERAL INFORMATION:
  APPLICANT: Ashkenazi, Avi J.
  APPLICANT: Baker, Kevin P.
  APPLICANT: Botstein, David
  APPLICANT: Desnovers, Luc
  APPLICANT: Eaton, Dan L.
  APPLICANT: Ferrara, Napoleone
  APPLICANT: Fogel, Sherman
  APPLICANT: Gershon, Peter
  APPLICANT: Gertzel, Mary E.
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul J.
  APPLICANT: Grimaldi, J. Christopher
  APPLICANT: Gurney, Austin L.
  APPLICANT: Klavin, Ivar J.
  APPLICANT: Knapier, Mary A.
  APPLICANT: Kohn, David
  APPLICANT: Pao, Nicholas F.
  APPLICANT: Roy, Margaret Ann
  APPLICANT: Stewart, Timothy A.
  APPLICANT: Tamas, Daniel
  APPLICANT: Williams, P. Mickey
  APPLICANT: Wood, William I.
  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
  FILE REFERENCE: P2730P1C20
  CURRENT APPLICATION NUMBER: US/09/592,598
  PRIORITY FILING DATE: 2001-11-14
  PRIOR APPLICATION NUMBER: 60/049787
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/062250
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/065186
  PRIOR FILING DATE: 1997-11-12
  PRIOR APPLICATION NUMBER: 60/065311
  PRIOR FILING DATE: 1997-11-13
  PRIOR APPLICATION NUMBER: 60/066770
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  PRIOR APPLICATION NUMBER: 60/075945
  PRIOR FILING DATE: 1998-02-25
  PRIOR APPLICATION NUMBER: 60/078910
  PRIOR FILING DATE: 1998-03-20
  PRIOR APPLICATION NUMBER: 60/083322
  PRIOR FILING DATE: 1998-04-28
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  PRIOR FILING DATE: 1998-05-07
  PRIOR APPLICATION NUMBER: 60/087106
  PRIOR FILING DATE: 1998-05-28
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  PRIOR APPLICATION NUMBER: 60/088028
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  PRIOR APPLICATION NUMBER: 60/088029
  PRIOR FILING DATE: 1998-06-04
  PRIOR APPLICATION NUMBER: 60/088030
  PRIOR FILING DATE: 1998-06-04
  PRIOR APPLICATION NUMBER: 60/088033

Query Match 100.0%; Score 20; DB 9; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 DRAT 4
Db 1 DRAT 4

RESULT 10
US-09-764-847-620
Sequence 620, Application US/09764847
GENERAL INFORMATION:
  APPLICANT: Ashkenazi, Avi J.
  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
  FILE REFERENCE: PC009
  CURRENT APPLICATION NUMBER: US/09/764,847
  PRIORITY FILING DATE: 2001-01-17
  PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
  NUMBER OF SEQ ID NOS: 2003
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO: 154
  LENGTH: 84
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: SITE
  LOCATION: (37)
  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
  NAME/KEY: SITE
  LOCATION: (81)
  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-620

Query Match 100.0%; Score 20; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy 1 DRAT 4
Db 1 DRAT 4

RESULT 11
US-09-992-598-274

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1 PRIOR FILING DATE: 1998-06-04  
2 PRIOR APPLICATION NUMBER: 60/088326  
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4 PRIOR APPLICATION NUMBER: 60/088167  
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7 PRIOR FILING DATE: 1998-06-05  
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9 PRIOR FILING DATE: 1998-06-05  
10 PRIOR APPLICATION NUMBER: 60/088217  
11 PRIOR FILING DATE: 1998-06-05  
12 PRIOR APPLICATION NUMBER: 60/088655  
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33 PRIOR FILING DATE: 1998-06-12  
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35 PRIOR FILING DATE: 1998-06-16  
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99 PRIOR FILING DATE: 1998-06-25  
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102 PRIOR APPLICATION NUMBER: 60/090863  
103 PRIOR FILING DATE: 1998-06-26  
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107 PRIOR FILING DATE: 1998-07-02  
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109 PRIOR FILING DATE: 1998-07-01  
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113 PRIOR FILING DATE: 1998-07-02  
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115 PRIOR FILING DATE: 1998-07-02  
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118 PRIOR APPLICATION NUMBER: 60/091982  
119 PRIOR FILING DATE: 1998-07-07  
120 PRIOR APPLICATION NUMBER: 60/092182  
121 PRIOR FILING DATE: 1998-07-09

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
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DB 74 DRAT 77

RESULT 12  
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; US/09989293A; P164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanov, David  
; APPLICANT: Deanov, David

1 APPLICANT: Eaton, Dan L.  
 2 APPLICANT: Erra, Napoleone  
 3 APPLICANT: Forster, Thomas  
 4 APPLICANT: Garber, Hanspeter  
 5 APPLICANT: Geriteen, Mary E.  
 6 APPLICANT: Goddard, Audrey  
 7 APPLICANT: Godowski, Paul J.  
 8 APPLICANT: Grimaldi, J. Christopher  
 9 APPLICANT: Gurney, Austin L.  
 10 APPLICANT: Harp, Jr., J.  
 11 APPLICANT: Napier, Mary A.  
 12 APPLICANT: Pan, James  
 13 APPLICANT: Paoni, Nicholas F.  
 14 APPLICANT: Roy, Margaret Ann  
 15 APPLICANT: Stewart, Timothy A.  
 16 APPLICANT: Tumas, Benjamin K.  
 17 APPLICANT: Williams, Colin K.  
 18 APPLICANT: Willm, P. Mickey  
 19 APPLICANT: Wood, William I.  
 20 APPLICANT: Zhang, Zemin  
 21  
 22 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 23  
 24 FILE REFERENCE: P27301C66  
 25  
 26 CURRENT APPLICATION NUMBER: US/09/989,293A  
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 28 PRIOR APPLICATION NUMBER: 60/001,400  
 29 PRIOR APPLICATION NUMBER: 60/045787  
 30 PRIOR FILING DATE: 1997-06-16  
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 77 PRIOR FILING DATE: 1998-06-19  
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 79 PRIOR APPLICATION NUMBER: 60/089948  
 80 PRIOR FILING DATE: 1998-06-19  
 81  
 82 PRIOR APPLICATION NUMBER: 60/089952  
 83 PRIOR FILING DATE: 1998-06-19  
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 85 PRIOR APPLICATION NUMBER: 60/090246  
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 95 PRIOR FILING DATE: 1998-06-23  
 96  
 97 PRIOR APPLICATION NUMBER: 60/090355  
 98 PRIOR FILING DATE: 1998-06-23  
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 100 PRIOR APPLICATION NUMBER: 60/090429  
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 103 PRIOR APPLICATION NUMBER: 60/090431  
 104 PRIOR FILING DATE: 1998-06-24  
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 106 PRIOR APPLICATION NUMBER: 60/090435  
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 110 PRIOR FILING DATE: 1998-06-24

1 PRIOR FILING DATE: 1998-06-24  
 2 PRIOR APPLICATION NUMBER: 60/090445  
 3 PRIOR FILING DATE: 1998-06-24  
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 5 PRIOR FILING DATE: 1998-06-24  
 6 PRIOR APPLICATION NUMBER: 60/090535  
 7 PRIOR FILING DATE: 1998-06-24  
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 9 PRIOR FILING DATE: 1998-06-24  
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 11 PRIOR FILING DATE: 1998-06-24  
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 13 PRIOR FILING DATE: 1998-06-24  
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 16 PRIOR APPLICATION NUMBER: 60/090676  
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 26 PRIOR APPLICATION NUMBER: 60/090862  
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 29 PRIOR FILING DATE: 1998-06-26  
 30 PRIOR APPLICATION NUMBER: 60/091360  
 31 PRIOR FILING DATE: 1998-07-01  
 32 PRIOR APPLICATION NUMBER: 60/091478  
 33 PRIOR FILING DATE: 1998-07-02  
 34 PRIOR APPLICATION NUMBER: 60/091544  
 35 PRIOR FILING DATE: 1998-07-02  
 36 PRIOR APPLICATION NUMBER: 60/091519  
 37 PRIOR FILING DATE: 1998-07-02  
 38 PRIOR APPLICATION NUMBER: 60/091626  
 39 PRIOR FILING DATE: 1998-07-02  
 40 PRIOR APPLICATION NUMBER: 60/091633  
 41 PRIOR FILING DATE: 1998-07-02  
 42 PRIOR APPLICATION NUMBER: 60/091978  
 43 PRIOR FILING DATE: 1998-07-02  
 44 PRIOR APPLICATION NUMBER: 60/091982  
 45 PRIOR FILING DATE: 1998-07-07  
 46 PRIOR APPLICATION NUMBER: 60/092182  
 47 PRIOR FILING DATE: 1998-07-09

Query Match Result 100.00; Score 20; DB 9; Length 86;

Sequence Similarity 100.00; Fred, No. 1.8e+02; Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
 DB 74 DRAT 77

RESULT 13  
 US-09-989-735-274  
 Sequence 274, Application US/09989735  
 Publication No. US20020193299A1  
 GENERAL INFORMATION:  
 1 APPLICANT: Ashkenazi, Avi J.  
 2 APPLICANT: Baker, Kevin P.  
 3 APPLICANT: Botstein, David  
 4 APPLICANT: Brown, David  
 5 APPLICANT: Brown, Dan L.  
 6 APPLICANT: Ferrara, Napoleone  
 7 APPLICANT: Fong, Sherman  
 8 APPLICANT: Garber, Hanspeter  
 9 APPLICANT: Geritsen, Mary E.  
 10 APPLICANT: Goddard, Audrey  
 11 APPLICANT: Godowski, Paul J.

1 APPLICANT: Grimaldi, J. Christopher  
 2 APPLICANT: Gurney, Austin L.  
 3 APPLICANT: Kijavini, Ivar J.  
 4 APPLICANT: Reptier, Mary A.  
 5 APPLICANT: Sen, James  
 6 APPLICANT: Roy, Nicholas P.  
 7 APPLICANT: Roy, Margaret Ann  
 8 APPLICANT: Stewart, Timothy A.  
 9 APPLICANT: Tumas, Daniel  
 10 APPLICANT: Metanabe, Colin K.  
 11 APPLICANT: Williams, P. Mickey  
 12 APPLICANT: Wood, William I.  
 13 APPLICANT: Wood, William I.  
 14 TITLE OF INVENTION: Secreted and Transmembrane Polypeptide-ides and Nucleic  
 15 ACIDS ENCODING THE SAME  
 16 TITLE REFERENCE: P27301C61  
 17 CURRENT APPLICATION NUMBER: US/09/989,735  
 18 CURRENT FILING DATE: 2001-11-19  
 19 PRIOR APPLICATION NUMBER: 60/049787  
 20 PRIOR FILING DATE: 1997-06-16  
 21 PRIOR APPLICATION NUMBER: 60/062250  
 22 PRIOR FILING DATE: 1997-10-17  
 23 PRIOR APPLICATION NUMBER: 60/065186  
 24 PRIOR FILING DATE: 1997-11-12  
 25 PRIOR APPLICATION NUMBER: 60/065311  
 26 PRIOR FILING DATE: 1997-11-13  
 27 PRIOR APPLICATION NUMBER: 60/066770  
 28 PRIOR FILING DATE: 1997-11-24  
 29 PRIOR APPLICATION NUMBER: 60/075945  
 30 PRIOR FILING DATE: 1998-02-25  
 31 PRIOR APPLICATION NUMBER: 60/078910  
 32 PRIOR FILING DATE: 1998-03-20  
 33 PRIOR APPLICATION NUMBER: 60/083322  
 34 PRIOR FILING DATE: 1998-04-28  
 35 PRIOR APPLICATION NUMBER: 60/084600  
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 37 PRIOR APPLICATION NUMBER: 60/087106  
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 40 PRIOR FILING DATE: 1998-06-02  
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 42 PRIOR FILING DATE: 1998-06-02  
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 45 PRIOR APPLICATION NUMBER: 60/087827  
 46 PRIOR FILING DATE: 1998-06-03  
 47 PRIOR APPLICATION NUMBER: 60/088021  
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 51 PRIOR APPLICATION NUMBER: 60/088026  
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 55 PRIOR APPLICATION NUMBER: 60/088029  
 56 PRIOR FILING DATE: 1998-06-04  
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 58 PRIOR FILING DATE: 1998-06-04  
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 60 PRIOR FILING DATE: 1998-06-05  
 61 PRIOR APPLICATION NUMBER: 60/088212  
 62 PRIOR FILING DATE: 1998-06-05  
 63 PRIOR APPLICATION NUMBER: 60/088217  
 64 PRIOR FILING DATE: 1998-06-05  
 65 PRIOR APPLICATION NUMBER: 60/088655  
 66 PRIOR FILING DATE: 1998-06-09  
 67 PRIOR APPLICATION NUMBER: 60/088734

/ PRIOR FILING DATE: 1998-06-10  
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 / PRIOR APPLICATION NUMBER: 60/089907  
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 / PRIOR APPLICATION NUMBER: 60/089948  
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 / PRIOR FILING DATE: 1998-06-24  
 / PRIOR APPLICATION NUMBER: 60/090444  
 / PRIOR FILING DATE: 1998-06-24  
 / PRIOR APPLICATION NUMBER: 60/090445  
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/ PRIOR APPLICATION NUMBER: 60/090540  
 / PRIOR FILING DATE: 1998-06-24  
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 / PRIOR APPLICATION NUMBER: 60/091478  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091544  
 / PRIOR FILING DATE: 1998-07-01  
 / PRIOR APPLICATION NUMBER: 60/091519  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091626  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091633  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091978  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/091982  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/092182  
 / PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 20; DB 9; Length 86;  
 Best Local Similarity 100.0%; Prod No. 18e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
 DB 74 DRAT 77

RESULT 14  
 US-09-930-444-274  
 / Sequence 274, Application US/0990444  
 / Publication No. US2002019300A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Ben-David, Eyal  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Saton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Kljavin, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas P.  
 / APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P270P1C19  
CURRENT APPLICATION NUMBER: US/09/990,444  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR APPLICATION NUMBER: 60/090676

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1 100.08; Score 20; DB 9; Length 86;
2 Best Local Similarity 100.08; Pred. No. 1,8e+02; Mismatches 0; Indels 0; Gaps 0;
3 Matches 4; Conservative 0;
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7 PRIOR FILING DATE: 1998-06-16  
8 PRIOR APPLICATION NUMBER: 60/089512  
9 PRIOR FILING DATE: 1998-06-16  
10 PRIOR APPLICATION NUMBER: 60/089514  
11 PRIOR FILING DATE: 1998-06-16  
12 PRIOR APPLICATION NUMBER: 60/089532  
13 PRIOR FILING DATE: 1998-06-17  
14 PRIOR APPLICATION NUMBER: 60/089538  
15 PRIOR FILING DATE: 1998-06-17  
16 PRIOR APPLICATION NUMBER: 60/089598  
17 PRIOR FILING DATE: 1998-06-17  
18 PRIOR APPLICATION NUMBER: 60/089599  
19 PRIOR FILING DATE: 1998-06-17  
20 PRIOR APPLICATION NUMBER: 60/089600  
21 PRIOR FILING DATE: 1998-06-17  
22 PRIOR APPLICATION NUMBER: 60/089653  
23 PRIOR FILING DATE: 1998-06-17  
24 PRIOR APPLICATION NUMBER: 60/089801  
25 PRIOR FILING DATE: 1998-06-18  
26 PRIOR APPLICATION NUMBER: 60/089907  
27 PRIOR FILING DATE: 1998-06-18  
28 PRIOR APPLICATION NUMBER: 60/089908  
29 PRIOR FILING DATE: 1998-06-19  
30 PRIOR APPLICATION NUMBER: 60/089947  
31 PRIOR FILING DATE: 1998-06-19  
32 PRIOR APPLICATION NUMBER: 60/089948  
33 PRIOR FILING DATE: 1998-06-19  
34 PRIOR APPLICATION NUMBER: 60/089952  
35 PRIOR FILING DATE: 1998-06-19  
36 PRIOR APPLICATION NUMBER: 60/090246  
37 PRIOR FILING DATE: 1998-06-20  
38 PRIOR APPLICATION NUMBER: 60/090252  
39 PRIOR FILING DATE: 1998-06-22  
40 PRIOR APPLICATION NUMBER: 60/090254  
41 PRIOR FILING DATE: 1998-06-22  
42 PRIOR APPLICATION NUMBER: 60/090349  
43 PRIOR FILING DATE: 1998-06-23  
44 PRIOR APPLICATION NUMBER: 60/090355  
45 PRIOR FILING DATE: 1998-06-23  
46 PRIOR APPLICATION NUMBER: 60/090429  
47 PRIOR FILING DATE: 1998-06-24  
48 PRIOR APPLICATION NUMBER: 60/090431  
49 PRIOR FILING DATE: 1998-06-24  
50 PRIOR APPLICATION NUMBER: 60/090435  
51 PRIOR FILING DATE: 1998-06-24  
52 PRIOR APPLICATION NUMBER: 60/090444  
53 PRIOR FILING DATE: 1998-06-24  
54 PRIOR APPLICATION NUMBER: 60/090445  
55 PRIOR FILING DATE: 1998-06-24  
56 PRIOR APPLICATION NUMBER: 60/090472  
57 PRIOR FILING DATE: 1998-06-24  
58 PRIOR APPLICATION NUMBER: 60/090535  
59 PRIOR FILING DATE: 1998-06-25  
60 PRIOR APPLICATION NUMBER: 60/090540  
61 PRIOR FILING DATE: 1998-06-24  
62 PRIOR APPLICATION NUMBER: 60/090542  
63 PRIOR FILING DATE: 1998-06-24  
64 PRIOR APPLICATION NUMBER: 60/090557  
65 PRIOR FILING DATE: 1998-06-24  
66 PRIOR APPLICATION NUMBER: 60/090676  
67 PRIOR FILING DATE: 1998-06-25  
68 PRIOR APPLICATION NUMBER: 60/090678  
69 PRIOR FILING DATE: 1998-06-25  
70 PRIOR APPLICATION NUMBER: 60/090690  
71 PRIOR FILING DATE: 1998-06-25  
72 PRIOR APPLICATION NUMBER: 60/090694  
73 PRIOR FILING DATE: 1998-06-25

Query Match 100.0%; Score 20; DB 9; Length 86;  
Best Local Similarity 100.0%; Pwd.No. 1.8e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

OY 1 DRAT 4  
DB 74 DRAT 77

Search completed: May 6, 2003, 15:04:53  
Job time : 9.33333 secs



Result	No.	Score	Query	DB	ID	Description
1	20	100.0	4	1	US-08-222-851-18	Sequence 18, Appl
2	20	100.0	16	2	US-08-797-842-3	Sequence 3, Appl
3	20	100.0	20	3	US-08-952-127-16	Sequence 16, Appl
4	20	100.0	19	4	US-08-952-127-16	Sequence 16, Appl
5	20	100.0	29	4	US-08-877-811-83	Sequence 13, Appl
6	20	100.0	4	2	US-08-797-842-11	Sequence 11, Appl
7	20	100.0	40	2	US-08-797-842-12	Sequence 12, Appl
8	20	100.0	44	1	US-07-956-7008-60	Sequence 60, Appl
9	20	100.0	44	1	US-08-476-537-60	Sequence 60, Appl
10	20	100.0	44	1	US-08-476-537-60	Sequence 60, Appl
11	20	100.0	44	2	US-08-476-537-60	Sequence 60, Appl
12	20	100.0	44	4	US-09-433-0438-360	Sequence 60, Appl
13	20	100.0	70	1	US-07-737-736B-3	Sequence 3, Appl
14	20	100.0	89	4	US-09-187-789-15	Sequence 15, Appl
15	20	100.0	89	4	US-09-139-600-10	Sequence 10, Appl
16	20	100.0	102	2	US-08-480-473B-51	Sequence 51, Appl
17	20	100.0	102	3	US-09-213-213-51	Sequence 51, Appl
18	20	100.0	102	3	US-09-213-213-51	Sequence 51, Appl
19	20	100.0	105	1	US-08-276-652-93	Sequence 93, Appl
20	20	100.0	105	1	US-08-276-652-93	Sequence 93, Appl
21	20	100.0	105	1	US-08-899-575-93	Sequence 93, Appl
22	20	100.0	105	5	US-08-899-575-93	Sequence 93, Appl
23	20	100.0	107	1	PT-US95-08743-93	Sequence 93, Appl
24	20	100.0	107	1	US-08-276-652-114	Sequence 114, Appl
25	20	100.0	107	1	US-08-899-575-114	Sequence 114, Appl
26	20	100.0	107	5	US-08-899-575-114	Sequence 114, Appl
27	20	100.0	107	5	PT-US95-08743-114	Sequence 114, Appl
28	20	100.0	108	1	US-08-276-682-98	Sequence 98, Appl

RESULT 2  
 US-08-797-842-3  
 ; Sequence 3, Application US/08/979842  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Martens, Koenraad et al  
 ; TITLE OF INVENTION: Antibodies specific for a haemostatic protein,  
 ; their use for isolating intact protein, haemostatic composition  
 ; TITLE OF INVENTION: of proteolytic cleavage products of the protein  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Martens, Koenraad and Wallace  
 ; STREET: Parkway 109 Office Center, 328 Newman Springs  
 ; STREET: Road, P. O. Box 8489  
 ; CITY: Red Bank  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07701  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: IBM PS/1, 2" 1.44 MByte IBM compatible diskette  
 ; OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11  
 ; SOFTWARE: Microsoft Word for Windows 6  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/797,842  
 ; FILING DATE: 10-Feb-1997  
 ; PRIORITY INFORMATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/381,891  
 ; FILING DATE: February 8, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Michaelson, Peter L.  
 ; REGISTRATION NUMBER: 30090  
 ; REFERENCE/DOCKET NUMBER: 30090  
 ; TELEPHONE: (908) 530-6671  
 ; TELEFAX: (908) 530-6584  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; TYPE: amino acid  
 ; LENGTH: 16 amino acids  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; US-08-797-842-3

Query Match 100.0%; Score 20; DB 2; Length 16;  
 Best Local Similarity 100.0%; Field No. 26;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 13 DRAT 16

RESULT 3  
 US-08-952-127-15  
 ; Sequence 16, Application US/08/952127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shiloh, Yosef  
 ; APPLICANT: Taglie, Danilo A.  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: INVARIANT, MARIA-TELANGELECTASIA GENE  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kohn & Associates  
 ; STREET: 30500 No. 6211336chwestern Hwy., Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan

COUNTRY: U.S.  
 ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/952,127  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,995  
 ; REFERENCE/DOCKET NUMBER: 2290,00029  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 810-539-5050  
 ; TELEFAX: 810-539-5055  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 21 amino acids  
 ; TYPE: amino acid

Query Match 100.0%; Score 20; DB 4; Length 19;  
 Best Local Similarity 100.0%; Field No. 31;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRAT 4  
 DB 7 DRAT 10

RESULT 4  
 US-08-952-127-13  
 ; Sequence 13, Application US/08/952127  
 ; Patent No. 6211336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shiloh, Yosef  
 ; APPLICANT: Taglie, Danilo A.  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: INVARIANT, MARIA-TELANGELECTASIA GENE  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kohn & Associates  
 ; STREET: 30500 No. 6211336chwestern Hwy., Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan  
 ; COUNTRY: U.S.  
 ; ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/952,127  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,995  
 ; REFERENCE/DOCKET NUMBER: 2290,00029  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 810-539-5050  
 ; TELEFAX: 810-539-5055  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 21 amino acids  
 ; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-952-127-13

Query Match      100.0%; Score 20; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4
DB 7 DRAT 10

RESULT 5
US-08-817-811-83
; Sequence 96; Application US/08817811
; Patent No. 5932706
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: B2
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FERC:005
; TELEPHONE: 512/418-3000
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: linear
US-08-817-811-83

Query Match      100.0%; Score 20; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4
DB 8 DRAT 11

RESULT 6
US-08-797-842-11
; Sequence 11; Application US/08797842
; Patent No. 5932706

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; GENERAL INFORMATION:
; APPLICANT: Mertens, Koenraad et al
; TITLE OF INVENTION: Antibodies specific for a haemostatic protein.
; TITLE OF INVENTION: their use for isolating intact protein, haemostatic composition
; TITLE OF INVENTION: of proteolytic cleavage products of the protein
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michaelson and Wallace
; STREET: Parkway 109 Office Center, 328 Newman Springs
; STREET: Parkway 109 Office Center, 328 Newman Springs
; CITY: Red Bank
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
; SOFTWARE: Microsoft Word for Windows 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,842
; FILING DATE: 10-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/381,891
; FILING DATE: 10-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaelson, Peter L.
; REGISTRATION NUMBER: 30090
; REFERENCE/DOCKET NUMBER: Stitching-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)530-6671
; TELEFAX: (908)530-6584
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYDROTHERMAL: NO
; INFORMATION FOR SEQ ID NO: 11:
; US-08-797-842-11

Query Match      100.0%; Score 20; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4
DB 25 DRAT 28

RESULT 7
US-08-797-842-12
; Sequence 12; Application US/08797842
; Patent No. 5932706
; GENERAL INFORMATION:
; APPLICANT: Mertens, Koenraad et al
; TITLE OF INVENTION: Antibodies specific for a haemostatic protein.
; TITLE OF INVENTION: their use for isolating intact protein, haemostatic composition
; TITLE OF INVENTION: of proteolytic cleavage products of the protein
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michaelson and Wallace
; STREET: Parkway 109 Office Center, 328 Newman Springs
; STREET: Parkway 109 Office Center, 328 Newman Springs
; CITY: Red Bank
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
; COMPUTER: IBM PC

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; OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11  
 ; SOFTWARE: Microsoft Word for Windows 6  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/797,842  
 ; CLASSIFICATION: 0-8D-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/381,891  
 ; FILING DATE: February 8, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Michaelson, Peter L.  
 ; REGISTRATION NUMBER: 30090  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 530-6671  
 ; TELEFAX: (908) 530-6584  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; LENGTH: 40 amino acids  
 ; STRANDEDNESS: acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; US-08-797-842-12

Query Match 100.0%; Score 20; DB 2; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRAT 4  
 DB 14 DRAT 17

RESULT 8  
 US-07-956-700B-60  
 ; Sequence 60, Application US/07956700B  
 ; Patent No. 5539092  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Haselkorn and Piotr Gornicki  
 ; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
 ; TITLE OF INVENTION: Carboxylase  
 ; NUMBER OF INVENTION: 116  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: 321 No. 553902th Clark Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/956,700B  
 ; CLASSIFICATION: 0-8D-1997  
 ; FILING DATE: 10/21/92  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Thomas E. No. 553902thrup  
 ; REGISTRATION NUMBER: 33,268  
 ; REFERENCE/DOCKET NUMBER: ARCD:058  
 ; TELEPHONE: 1-312-755-4489  
 ; TELEFAX: 1-312-755-4489  
 ; INFORMATION FOR SEQ ID NO: 60:  
 ; LENGTH: 44 amino acids  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear

; MOLECULE TYPE: Peptide  
 ; US-07-956-700B-60

Query Match 100.0%; Score 20; DB 1; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRAT 4  
 DB 25 DRAT 28

RESULT 9  
 US-07-956-700B-60  
 ; Sequence 60, Application US/08476537  
 ; Patent No. 5756290  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Haselkorn and Piotr Gornicki  
 ; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
 ; TITLE OF INVENTION: Carboxylase  
 ; NUMBER OF INVENTION: 116  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: 321 No. 5756290th Clark Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60610  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/476,537  
 ; FILING DATE: 10/21/92  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Thomas E. No. 5756290thrup  
 ; REGISTRATION NUMBER: 33,268  
 ; REFERENCE/DOCKET NUMBER: ARCD:058  
 ; TELEPHONE: 1-312-755-4489  
 ; TELEFAX: 1-312-755-4489  
 ; INFORMATION FOR SEQ ID NO: 60:  
 ; LENGTH: 44 amino acids  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Peptide  
 ; US-08-476-537-60

Query Match 100.0%; Score 20; DB 1; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRAT 4  
 DB 25 DRAT 28

RESULT 10  
 US-08-485-607-60  
 ; Sequence 60, Application US/08485607  
 ; Patent No. 5792627  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Haselkorn and Piotr Gornicki  
 ; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
 ; TITLE OF INVENTION: Carboxylase

```

; NUMBER OF SEQUENCES: 116
; CONTACT ADDRESS: 321 No. 5792644 5786170thrup
; ADDRESSEE: A. Robert Haselkorn, Robert Gornicki
; STREET: 321 No. 5792644 5786170thrup
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.607
; FILING DATE: 07-JUN-1995
; PRIORITY DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD.058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-755-4489
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-485-607-60

Query Match 100.0%; Score 20; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4
Db 25 DRAT 28

RESULT 11
US-08-475-879-60
; Sequence 60, Application US/08475879
; Patent No. 5792644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: A. Robert Haselkorn, Robert Gornicki
; STREET: 321 No. 5792644 5786170thrup
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475.879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700

Query Match 100.0%; Score 20; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4
Db 25 DRAT 28

RESULT 11
US-08-475-879-60
; Sequence 60, Application US/08475879
; Patent No. 5792644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: A. Robert Haselkorn, Robert Gornicki
; STREET: 321 No. 5792644 5786170thrup
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475.879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700

Query Match 100.0%; Score 20; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4
Db 25 DRAT 28

RESULT 12
US-09-433-043B-60
; Sequence 60, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
; FILED FOR INVENTION: 1999-10-25
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQUENCES: 116
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 60
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; INFORMATION: Peptide
; US-09-433-043B-60

Query Match 100.0%; Score 20; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRAT 4
Db 25 DRAT 28

RESULT 13
US-07-737-736B-3
; Sequence 3, Application US/07737736B
; Patent No. 5260199
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: ROSE, TROY K.
; APPLICANT: PRAHL, JEAN M.
; TITLE OF INVENTION: Method of Producing
; TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady  
 STREET: 411 East Wisconsin Avenue  
 CITY: Milwaukee  
 STATE: Wisconsin  
 COUNTRY: U.S.A.  
 ZIP: 53202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 19910730  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Schwartz, Carl R.  
 REGISTRATION NUMBER: 29,437  
 REFERENCE/DOCKET NUMBER: 96-296-2185-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 414-277-5115  
 TELEFAX: 414-277-5774  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 70 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULAR TYPE: protein  
 HYDROTICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Chicken  
 PUBLICATION INFORMATION:  
 AUTHORS: McDonnell, Donald P.  
 AUTHORS: Engelsgood, David J.  
 AUTHORS: Pridmore, R. W.  
 AUTHORS: Hausler, Mark R.  
 AUTHORS: O'Malley, Bert W.  
 TITLE: Molecular Cloning of Complementary DNA  
 JOURNAL: Science  
 VOLUME: 232  
 PAGES: 1218-1217  
 DATE: March 6-1987

US-07-737-736B-3  
 Query Match 100.0%; Score 20; DB 1; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
 DB 8 DRAT 11

RESULT 14  
 US-09-187-789-15  
 Sequence 15, Application US/09187789  
 Patent No. 6340740  
 GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emad S.  
 APPLICANT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 TITLE OF INVENTION: METHODS OF USE  
 REFERENCE: 480140.34C1  
 CURRENT FILING DATE: 1998-11-06  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 15  
 LENGTH: 89  
 TYPE: PRT

ORGANISM: Mus musculus  
 US-09-187-789-15  
 Query Match 100.0%; Score 20; DB 4; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78  
 RESULT 15  
 US-09-139-600-10  
 Sequence 10, Application US/09139600  
 Patent No. 6432628  
 GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emad S.  
 APPLICANT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 TITLE OF INVENTION: AND METHOD OF USE  
 REFERENCE: 480140.34C1  
 CURRENT FILING DATE: 1998-08-25  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 10  
 LENGTH: 89  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-139-600-10  
 Query Match 100.0%; Score 20; DB 4; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 DB 75 DRAT 78  
 Search completed: May 6, 2003, 15:04:06  
 Job time : 7.4 secs

GenCore version 5.1.4.P5.4578  
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OM protein - protein search, using sw model

Run on: May 6, 2003, 14:57:44 ; Search time 18.2 Seconds  
(without alignments)  
29.286 Million cell updates/sec

Title: US-09-851-422b-2

Perfect score: 20

Sequence: 1 DEAT 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	20	100.0	4	16	AA83079
2	20	100.0	12	21	AA83079
3	20	100.0	15	15	AA830057
4	20	100.0	16	15	AA830113
5	20	100.0	19	18	AAW36170
6	20	100.0	19	20	AAW01771
7	20	100.0	21	18	AAW07660
8	20	100.0	21	22	AA878221
9	20	100.0	22	17	AA897470
10	20	100.0	28	17	AA891591

11	20	100.0	36	22	AA873731	Human colon cancer
12	20	100.0	37	21	AA93158	Human K562 cell re
13	20	100.0	38	21	AA856794	Human K562 cell re
14	20	100.0	38	21	AA856794	Arabidopsis thalia
15	20	100.0	38	22	AA857857	Human immune haema
16	20	100.0	40	21	AA832462	Human secreted pro
17	20	100.0	43	22	AB811187	Human pheromone re
18	20	100.0	44	20	AAW74045	Human D2H binding
19	20	100.0	46	12	AA810755	Non-A non-B hepati
20	20	100.0	46	12	AA810755	Arabidopsis thalia
21	20	100.0	50	22	AAU77589	Human K562 cell re
22	20	100.0	50	22	AAU77589	Human K562 cell re
23	20	100.0	52	22	AAU52605	Taxus cuspidata RT
24	20	100.0	53	22	AAU56447	Propionibacterium
25	20	100.0	54	22	AAU55929	Propionibacterium
26	20	100.0	54	22	AAU60960	Propionibacterium
27	20	100.0	54	22	AAU62528	Propionibacterium
28	20	100.0	54	22	AAU62528	Propionibacterium
29	20	100.0	57	22	AAU67182	Propionibacterium
30	20	100.0	57	22	AB811792	Peptide #4443 enco
31	20	100.0	57	22	AB811792	Peptide #4527 enco
32	20	100.0	57	22	AB816368	Human nervous syst
33	20	100.0	57	22	AB822336	Protein #4335 enco
34	20	100.0	57	22	AAW57748	Human brain expres
35	20	100.0	57	22	AAW70162	Human bone marrow
36	20	100.0	57	22	AAW70162	Human bone marrow
37	20	100.0	57	22	AAW70162	Peptide #4443 enco
38	20	100.0	57	22	AAW56227	Peptide #4533 enco
39	20	100.0	57	23	AB839799	Human peptide enco
40	20	100.0	57	23	ABP42618	Human ovarian anti
41	20	100.0	58	22	AAW75801	Human colon cancer
42	20	100.0	59	21	AA840924	Human ORFX ORF688
43	20	100.0	59	21	AA801585	Human secreted pro
44	20	100.0	59	21	AA801585	Human secreted pro
45	20	100.0	60	22	AAU67029	Propionibacterium

#### ALIGNMENTS

RESULT 1  
AA83079  
ID AA83079 standard; peptide; 4 AA.  
AC AA83079;  
DT 16-MAY-1996 (first entry)  
DE Class I MHC antigen alpha-1 domain tetrapeptide #3.  
DE Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
DE immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW class I MHC.  
XX Synthetic.  
XX W09526979-A1.  
XX 12-OCT-1995.  
XX 05-APR-1995; 95WO-US04349.  
XX 05-APR-1994; 94US-0222851.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX Clayberger C, Krenaky AM, Parham P;  
XX WPI; 1995-358582/46.  
XX Extension of acceptance period of transplants from MHC unmatched  
XX donor hosts - using Class I B75-84 MHC antigen of the recipient  
XX host





XX SQ Sequence 12 AA;  
Query Match 100.0%; Score 20; DB 21; Length 12;  
Best Local Similarity 100.0%; Prd. No. 59;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRAT 4  
4 DRAT 7

Db 4 DRAT 7

RESULT 4  
AAAS0113  
ID AAS0113 standard; peptide; 16 AA.  
XX  
AC AAS0113;  
KT AAS0113;  
DT 07-OCT-1994 (first entry)  
XX  
DE Peptide reactive with antibody specific for factor IX.  
XX Polypeptide; peptide; oligopeptide; factor IX; haemostatic protein;  
KW antibody; treatment; haemostatic disease; thromboembolic disease.  
XX Homo sapiens.  
XX W09405692-A.  
XX  
PN 17-MAR-1994.  
XX  
PD 26-AUG-1993; 93MO-NL00174.  
XX  
PF 27-AUG-1992; 92EP-0202615.  
XX  
PR (BLOB-) STICHTING CENT LAB VAN DE BLOEDTRANSFUSI.  
XX  
PA Mertens K, Van Mourik JA;  
PI WPI; 1994-101117/12.  
XX  
DR Isolating haemostatic proteins free of proteolytic degradation  
PT products - using new antibodies which distinguish between intact  
PT and cleaved forms of the protein, useful in treatment of  
PT haemostatic diseases  
XX  
PS Claim 6; Page 25; 32pp; English.  
XX The polypeptide can be used to screen antibodies to select  
XX a substance that interferes with the function of factor IX and can  
XX substantially distinguish between intact and cleaved species of the  
XX haemostatic protein. The polypeptide corresponds to amino acid  
XX residues 320-335 of factor IX. Haemostatic proteins are used in the  
XX treatment of haemostatic e.g. thromboembolic diseases. See  
XX AAAS0111-R50114.  
XX

XX SQ Sequence 16 AA;  
Query Match 100.0%; Score 20; DB 15; Length 16;  
Best Local Similarity 100.0%; Prd. No. 80;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRAT 4  
13 DRAT 16

Db 13 DRAT 16

RESULT 5  
AAW36170  
ID AAW36170 standard; peptide; 19 AA.  
XX  
AC AAW36170;  
XX  
XX

DT 30-MAR-1998 (first entry)  
XX Mouse ATM gene product epitope 1.  
XX Ataxia-telangiectasia; A-T; mutated; ATM; 11q22-23; signal transduction;  
KW DNA damage; cell cycle control; screening; gene therapy; catalytic;  
KW phosphatidylinositol-3 kinase; PI-3; cancer predisposition; carrier;  
KW untranslated region; UTR.  
XX  
XX Mus sp.  
XX W09636695-A1.  
XX  
PN 21-NOV-1996.  
XX  
PD 16-MAY-1996; 96WO-US07040.  
XX  
PF 26-JUL-1995; 95US-0608936.  
XX  
PR 12-MAY-1995; 95US-0449822.  
XX  
PR 21-JUN-1995; 95US-0493092.  
XX  
PA (UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Collins FS, Shiloh Y, Tagle DA;  
PI WPI; 1997-012074/01.  
XX  
XX New gene ATM implicated in ataxia-telangiectasia and related protein  
PT - useful in screening methods, partic. for identifying disease  
carriers  
XX  
XX Claim 24; Page 105; 127pp; English.  
XX  
XX AAW36170-72 are mouse ATM protein epitopes used to generate polyclonal  
CC antibodies. Antibodies raised against the ATM protein detected  
CC mono-specifically a high molecular weight of the expected size of 350  
CC kDa on Western blots of protein lysates derived from fibroblast and  
CC lympho- blastoid cell lines. Because of the high frequency of truncation  
CC mutations in the ATM gene, mutated ATM protein can be identified if such  
CC proteins are stable. Mutations in the ATM gene cause ataxia-  
CC telangiectasia (A-T), a progressive genetically disorder affecting the  
CC nervous system and a variety of other organs. A novel signal transduction system  
CC 11q22-23 is probably involved in a novel signal transduction system  
CC that links DNA damage surveillance to cell cycle control. The ATM gene  
CC product (AAW07655) has a highly conserved C-terminal region showing high  
CC sequence homology to the catalytic domain of phosphatidylinositol-3  
CC kinases. A-T mutations affect a variety of tissues and lead to cancer  
CC predisposition. Identification of A-T carriers, by analysis at nucleic  
CC acid of protein levels, allows better supervision and treatment of such  
CC carriers. Transgenic mice have been generated and used for the study of  
CC particularly sensitive to radiation. The transgenic animals and  
CC transformed cells are useful as models of the human disease. Also viral  
CC vectors expressing the ATM protein can be used in gene therapy of A-T.  
XX

XX SQ Sequence 19 AA;  
Query Match 100.0%; Score 20; DB 18; Length 19;  
Best Local Similarity 100.0%; Prd. No. 96;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRAT 4  
7 DRAT 10

Db 7 DRAT 10

RESULT 6  
AAV01771  
ID AAV01771 standard; peptide; 19 AA.  
XX  
AC AAV01771;  
XX  
XX 28-JUN-1999 (first entry)  
DT

XX DE M-ras derived antigenic peptide used to raise antibodies.  
 XX PA M-ras; interleukin-9 signaling pathway; pathogenesis; atopic allergy;  
 XX KW aschma; leukemia; lymphoma; tumor; T-cell lymphoma; Hodgkin's disease;  
 XX KW mycosis fungoides.  
 XX OS Unidentified.  
 XX OS Unidentified.  
 XX PN W09914242-A2.  
 XX PD 25-MAR-1999.  
 XX PD 18-SEP-1998; 98WO-US19625.  
 XX PD 19-SEP-1997; 97US-0059509.  
 XX PR (MAGA-) MAGAININ PHARM INC.  
 XX PA Grasso L, Levitt R, Loughed J, Nicolaides N, Renauld J;  
 XX PI WPT; 1999-244027/20.  
 XX XX Nucleic acid encoding human or murine M-Ras  
 XX PT Disclosure; Page 17; 69pp; English.  
 XX PS The present sequence represents a peptide derived from M-ras  
 XX CC protein, which was used to raise antibodies. M-Ras is a part of  
 XX CC the Ras family of proteins. Ras is involved in the regulation of  
 XX CC atopic allergy, asthma and similar conditions. Some leukemias and  
 XX CC lymphomas and tumors. Agents that downregulate M-Ras are used to  
 XX CC treat these conditions, particularly T-cell lymphoma or leukemia;  
 XX CC Hodgkin's disease and mycosis fungoides. Measuring levels of M-Ras  
 XX CC is used to diagnose, or monitor, these conditions (an elevated level  
 XX CC being indicative of disease).  
 XX CC  
 XX SQ Sequence 19 AA;  
 Query Match 100.0%; Score 20; DB 20; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 I I I I  
 DB 10 DRAT 13  
 RESULT 7  
 AAM07660  
 ID AAM07660 standard; Peptide; 21 AA.  
 XX AC  
 XX AC AAM07660;  
 XX DT 30-MAR-1998 (first entry)  
 XX DE Human ATM gene product epitope 5.  
 XX KW Ataxia-telangiectasia; A-T; mutated; ATM; 11q22-23; signal transduction;  
 XX KW DNA damage; cell cycle control; autophagy; gene therapy; cancer;  
 XX KW protein kinase C; protein kinase B; protein kinase C; protein kinase C;  
 XX KW untranslated region; UTR.  
 XX OS Homo sapiens.  
 XX OS WO9636695-A1.  
 XX PN 21-NOV-1996.  
 XX PD 16-MAY-1996; 96MO-US07040.  
 XX PR 28-JUL-1995; 95US-0508836.  
 XX PR 16-MAY-1995; 95US-0441822.

PR 21-JUN-1995; 95US-0493092.  
 XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.  
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX AC Collins FS, Shiloh Y, Tagle DA,  
 XX DT WPI; 1997-012074/01.  
 XX DE New gene ATM implicated in ataxia-telangiectasia and related protein  
 XX PT - useful in screening methods, partic. for identifying disease  
 XX carriers  
 XX Example 5; Page 104; 127pp; English.  
 XX PS AAM07656-62 are human ATM protein epitopes used to generate polyclonal  
 XX CC and monoclonal antibodies. Antibodies raised against the ATM protein  
 XX CC detected mono-specifically a high molecular weight of the expected size  
 XX CC of 350 kDa on Western blots of protein lysates derived from fibroblast  
 XX CC and lympho-blastoid cell lines. Because of the high frequency of  
 XX CC mutations in the ATM gene, the antibodies were used to identify  
 XX CC individuals affected if such proteins are stable. Mutations in the ATM gene cause  
 XX CC ataxia-telangiectasia (A-T), a progressive genetic disorder affecting  
 XX CC the central nervous and immune systems. The ATM gene, located at  
 XX CC chromosome 11q22-23, is probably involved in a novel signal transduction  
 XX CC system that links DNA damage surveillance to cell cycle control. The ATM  
 XX CC gene product (AAM07655) has a highly conserved C-terminal region showing  
 XX CC high sequence homology to the catalytic domain of phosphatidylinositol-3  
 XX CC kinase (PI-3K). The identification of A-T carriers by analysis at nucleic  
 XX CC acid or protein levels, allows better supervision and treatment of such  
 XX CC subjects who are at increased risk of developing cancer and are  
 XX CC particularly sensitive to radiation. The transgenic animals and  
 XX CC transformed cells are useful as models of the human disease. Also viral  
 XX CC vectors expressing the ATM protein can be used in gene therapy of A-T.  
 XX CC  
 XX SQ Sequence 21 AA;  
 Query Match 100.0%; Score 20; DB 18; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 11e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRAT 4  
 I I I I  
 DB 7 DRAT 10  
 RESULT 8  
 AAB87221  
 ID AAB87221 standard; Peptide; 21 AA.  
 XX AC  
 XX AC AAB87221;  
 XX DT 10-MAY-2001 (first entry)  
 XX DE Breast-cancer associated protein isoform BPI-20 peptide #2.  
 XX KW Human; breast cancer; breast cancer associated protein isoform BPI;  
 XX KW breast cancer associated feature; BPI; diagnosis; cytosolic.  
 XX OS Homo sapiens.  
 XX OS WO200113117-A2.  
 XX PN 22-FEB-2001.  
 XX PD 14-AUG-2000; 2000WO-G03143.  
 XX PR 13-AUG-1999; 99GB-0019258.  
 XX PR 30-MAR-2000; 2000GB-0007754.  
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC;  
 XX WPI, 2001-211252/21.  
 XX  
 XX Screening, diagnosis or prognosis of breast cancer, by analyzing a  
 XX sample of serum or plasma by two dimensional electrophoresis to detect  
 XX the presence or level of a breast cancer-associated feature  
 XX  
 XX Disclosure; Page 25; 146pp; English.  
 XX  
 XX The present invention describes a method for the screening, diagnosis or  
 XX prognosis of breast cancer (BC), determining the stage or severity of BC,  
 XX and monitoring the effect of therapy administered to a subject having BC,  
 XX comprising analysing a sample of body fluid by two dimensional  
 XX electrophoresis to generate a two-dimensional array of features,  
 XX comprising a chosen feature whose abundance correlates with BC or  
 XX predicts the onset or course of BC. The method (I) involves:  
 XX (a) analysing a body fluid from a subject having a two-dimensional  
 XX electrophoresis to generate two-dimensional features;  
 XX comprising a chosen feature whose relative abundance correlates with BC  
 XX or predicts the onset of BC; and (b) comparing the abundance of each  
 XX chosen feature in the sample with the abundance of that chosen feature  
 XX in the body fluid from one or more persons free from BC, or with a  
 XX previously determined reference range for that feature in subjects free  
 XX from BC, or with the abundance of an expression reference feature (ERF)  
 XX in the sample. The methods are useful for screening, diagnosis or  
 XX prognosis of breast cancer, and for identifying a subject at risk of BC,  
 XX monitoring the effect of therapy administered to a subject having BC,  
 XX and for identifying a subject at risk of developing BC. AA87186 to  
 XX AA87370 represents breast cancer associated protein isoform (BPT)  
 XX peptide sequences, and AA91643 to AA91848 represent BPT probes used in  
 XX the exemplification of the present invention.  
 XX  
 XX Sequence 21 AA;  
 XX  
 XX Query Match 100.0%; Score 20; DB 22; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Oy 1 DRAT 4  
 XX |||||  
 XX Db 9 DRAT 12  
 XX  
 XX RESULT 9  
 XX AA87370  
 XX ID AA897470 standard; peptide; 28 AA.  
 XX AC AA897470;  
 XX DT AA897470;  
 XX DE 04-DEC-1996 (first entry)  
 XX DE Chimeric peptide be41 contg. C. elegans unc-15 paraymosin peptide.  
 XX KW Paraymosin protein; peptide; unc-15; chimeric; chimeric;  
 XX KW B-cell; conformational epitope; alpha-helix; GC4; leucine zipper;  
 XX KW detection; mapping; opsonic antibody; vaccine; immunotherapy;  
 XX KW diagnosis.  
 XX OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX FH Peptide 8..22  
 XX FT notes "unc-15 conformational B-cell epitope"  
 XX FT  
 XX PK WO9611944-A1.  
 XX PD 25-APR-1996.  
 XX PF 16-OCT-1995; 95MO-AU00681.  
 XX PF 14-OCT-1994; 94AU-0008851.  
 XX PI Fowles DW, Rodwell JD;  
 XX  
 XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
 XX (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
 XX (COOR-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX (UIME-) UNIV MELBOURNE.  
 XX  
 XX Cooper JA, Good MF, Relf WA, Saul AJ;  
 XX WPI, 1996-221939/22.  
 XX  
 XX New chimeric peptide(s) including a conformational epitope -  
 XX inserted into a peptide having similar native conformation, useful  
 XX in vaccines and for determ. of minimal epitope(s) or for mapping  
 XX amphipathic helices  
 XX  
 XX Example 18; Page 45; 99pp; English.  
 XX  
 XX The present peptide is a chimeric peptide (CP), contg. a  
 XX C. elegans unc-15 paraymosin peptide. The CP comprises a B-cell  
 XX conformational epitope from within unc-15, inserted into a 2nd  
 XX peptide, pref. an alpha-helical coil based on the GC4 leucine  
 XX zipper peptide (AA87395). The 2nd peptide has a similar  
 XX conformation, enabling the epitope to be presented in an  
 XX immunologically active conformation.  
 XX The CP can be used in a novel detection/mapping process, e.g. to  
 XX determine the effect of therapy administered to a subject having BC,  
 XX (AA87370) and in vaccing against C. elegans Ab raised against the CP  
 XX can be used for immunotherapy and diagnosis, while the CP can be  
 XX used diagnostically to detect Ab.  
 XX  
 XX Sequence 28 AA;  
 XX  
 XX Query Match 100.0%; Score 20; DB 17; Length 28;  
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Oy 1 DRAT 4  
 XX |||||  
 XX Db 8 DRAT 11  
 XX  
 XX RESULT 10  
 XX AA91391  
 XX ID AA891391 standard; Peptide; 28 AA.  
 XX AC AA891391;  
 XX DT 10-OCT-1996 (first entry)  
 XX DE ME81 library derived peptide, F15-A9b.  
 XX KW Cis-element; ligand; highly specific DNA binding domain; HSDB; human;  
 XX KW H2-kappa-B; regulatory domain; murine; homologue; IL-6; interleukin;  
 XX KW HLA class I gene; HLA-B\*27; HLA-J; HLA-A2; acute phase protein response;  
 XX KW syngene; immune response; IL-8; IL-16; diagnosis; gene therapy;  
 XX KW transcription.  
 XX OS Synthetic.  
 XX  
 XX WO9606188-A1.  
 XX PN 29-FEB-1996.  
 XX PD 17-AUG-1995; 95WO-US10523.  
 XX PF 15-AUG-1995; 95US-0515190.  
 XX PR 18-AUG-1994; 94US-0292902.  
 XX XX (CYTO-) CYTOGEN CORP.  
 XX PA Fowles DW, Rodwell JD;  
 XX PI

DR WPI; 1996-151391/15.  
 XX Synthetic random nucleotide sequences encoding ligand binding  
 PT domains - identified by screening library of vectors or peptide (s)  
 PT and useful for gene therapy and diagnosis  
 XX Claim 70; Page 196; 224pp; English.  
 PS The sequences given in AAG7378-414 represent peptides that bind to  
 CC highly specific DNA binding domains (HSDB)'s. These sequences were  
 CC tested for binding to the H2-kappa-B oligonucleotide which contains  
 CC the NF-kappa-B binding site, and comprises the sequence given in  
 CC AAG7379. These peptides may be used in a composition for diagnosis and  
 CC gene therapy and for modifying the transcription or activity of a gene.  
 XX Sequence 28 AA;  
 SQ

Query Match 100.0%; Score 20; DB 17; Length 28;  
 Best Local Similarity 100.0%; Fred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DRAT 4  
 DB 12 DRAT 15

RESULT 11  
 AAG73731 standard; Protein; 36 AA.  
 XX AAG73731  
 AC AAG73731;  
 XX  
 DT 03-SEP-2001 (first entry)  
 DE Human colon cancer antigen protein SEQ ID NO:4495.  
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma.  
 XX Homo sapiens.  
 OS  
 XX WO200122920-A2.  
 PN  
 XX 05-APR-2001.  
 PD  
 XX 28-SEP-2000; 2000WO-UG26524.  
 PF  
 XX 29-SEP-1999; 99US-0157137.  
 PR  
 XX 03-NOV-1999; 99US-0163280.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PI WPI; 2001-235357/24.  
 DR N-PSDB; AAG73162.  
 XX

Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 useful for preventing, diagnosing and/or treating colorectal cancers -  
 AAG73162; English.  
 Claim 11; Page 6295; 9801pp; English.  
 XX AAG73943 to AAG73195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and treatment of diseases associated with inactivation of P  
 CC diagnosis and treatment of diseases associated with inactivation of P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patient's own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated P,

CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAG7196 to AAG7204  
 CC and AAG77789 represent sequences used in the exemplification of the  
 CC present invention. 682 and page 7053 of the sequence listing were  
 CC mispaginated. The sequences given in the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX Sequence 36 AA;  
 SQ

Query Match 100.0%; Score 20; DB 22; Length 36;  
 Best Local Similarity 100.0%; Fred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DRAT 4  
 DB 28 DRAT 31

RESULT 12  
 AAY93158 standard; peptide; 37 AA.  
 ID AAY93158  
 XX AAY93158;  
 AC AAY93158;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX Human vitamin D receptor amino acids 18-54.  
 XX Cytosolic; mutant; mutain; oestrogen receptor-alpha; zinc finger;  
 KW oestrogen receptor-beta; vitamin D receptor; retinoic acid receptor;  
 KW thyroid hormone receptor; proliferation; motility; invasiveness; cancer;  
 KW breast; ovary.  
 XX  
 XX Homo sapiens.  
 XX WO200035955-A1.  
 PN  
 XX 22-JUN-2000.  
 PD  
 XX 17-DEC-1999; 99WO-FR03173.  
 PF  
 XX 17-DEC-1998; 98FR-0015922.  
 PR  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA  
 XX Garcia M, Platet N, Rochefort H;  
 PI WPI; 2000-442369/38.  
 DR

Composition containing nucleic acid encoding variant estrogen receptor  
 XX useful for treating or preventing cancer -  
 XX Example 2; Fig 3; 33pp; French.  
 PS

The invention relates to a pharmaceutical composition containing at  
 CC least a nucleic acid encoding a variant estrogen receptor that  
 CC encodes a zinc finger domain (zinc finger) but which lacks the ability to bind estrogen and/or AP-2 (a  
 CC transcriptional activator). The variation is especially in the region  
 CC comprising amino acid 179-215 of the alpha estrogen receptor. Similar  
 CC variations may be generated in the homologues of other estrogen-type  
 CC receptor such as estrogen receptor-beta, vitamin D receptor, retinoic  
 CC acid receptor or thyroid hormone receptor (see peptides  
 CC AAY352923158 to AAY352923159). The receptor domain is therefore  
 CC amino acid 179-215 of the receptor domain. The receptor is therefore  
 CC present cancer, specifically of the breast or ovary.  
 XX Sequence 37 AA;  
 SQ

Query Match 100.0%; Score 20; DB 21; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
DB 12 DRAT 15

# RESULT 13

AA164710.  
AA164710 standard; Protein, 37 AA.

AC AAV64710;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:871.  
DE Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;  
KW gene therapy; chromosome mapping; upstream regulatory sequence;  
KW forensic; location; development; protein synthesis; stability;  
KW regulation; identification.

XX Homo sapiens.

XX W09953051-A2.

XX 21-OCT-1999.

XX 09-APR-1999; 99MO-IB00712.

XX 09-APR-1998; 99US-0057719.

XX 28-APR-1998; 99US-0069047.

XX (GENSET) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX MPI; 2000-038446/03.

XX N-FSDB; AA242324.

XX Novel secreted protein 5' expressed sequence tag sequences used in  
diagnostic, forensic, gene therapy, and chromosome mapping procedures

XX Claim 3; Page 618; 837pp; English.

XX AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)  
sequences, corresponding to human secreted proteins. AA164651 to  
AA164658 represent the EST-related proteins corresponding to AA242265 to  
AA164658. The ESTs are used to identify and isolate human gene  
products. They can be used to identify and isolate human gene  
products (UTRs) and upstream regulatory regions which control the  
location, development, stage, rate, and quantity of protein synthesis, as  
well as stability of mRNA. The ESTs are also useful as probes for  
chromosome mapping, and to obtain full length cDNA clones. The ESTs can  
also be used in forensic procedures to identify individuals, or in  
diagnostic procedures to identify individuals having genetic diseases  
associated with the gene products. The nucleic acids encoding signal peptides can be  
used for directing extracellular secretion of a polypeptide or the  
insertion of a polypeptide into a membrane, or importing a polypeptide  
into a cell. The proteins encoded by the EST sequences may be useful in  
treating a variety of human conditions. Secreted proteins have  
therapeutic value, and the identification of new secreted proteins is  
valuable. AA242265 to AA242268 and AA164644 to AA164650 represent  
sequences used in the exemplification of the present invention.

XX Sequence 37 AA;

XX Query Match

XX Best Local Similarity 100.0%; Score 20; DB 21; Length 37;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRAT 4  
DB 33 DRAT 36

# RESULT 14

AA656794.  
AA656794 standard; Protein, 38 AA.

AC AAG56794;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 73090.

DE Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridization assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0125788.

XX 23-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126795.

XX 01-APR-1999; 99US-0127352.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129645.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 24-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131044.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0132918.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 24-MAY-1999; 99US-0135639.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 08-JUN-1999; 99US-0138064.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 18-JUN-1999; 99US-0139861.  
PR 18-JUN-1999; 99US-0139862.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 23-JUN-1999; 99US-0140355.  
PR 24-JUN-1999; 99US-0140693.  
PR 24-JUN-1999; 99US-0140823.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141342.  
PR 01-JUL-1999; 99US-0141254.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142820.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143342.  
PR 15-JUL-1999; 99US-0143342.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145224.  
PR 27-JUL-1999; 99US-0145591.  
PR 27-JUL-1999; 99US-0145591.  
PR 27-JUL-1999; 99US-0145591.  
PR 27-JUL-1999; 99US-0145591.  
PR 28-JUL-1999; 99US-0145591.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0147033.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147303.  
PR 09-AUG-1999; 99US-0147446.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148564.

PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 21-AUG-1999; 99US-0149723.  
PR 21-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0150566.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151069.  
PR 27-AUG-1999; 99US-0151070.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 01-SEP-1999; 99US-0152363.  
PR 07-SEP-1999; 99US-0153070.  
PR 10-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 15-SEP-1999; 99US-0154018.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 04-OCT-1999; 99US-0157117.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158039.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0158293.  
PR 13-OCT-1999; 99US-0158294.  
PR 13-OCT-1999; 99US-0158294.  
PR 13-OCT-1999; 99US-0158294.  
PR 14-OCT-1999; 99US-0159310.  
PR 14-OCT-1999; 99US-0159310.  
PR 14-OCT-1999; 99US-0159311.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
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PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160982.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 25-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161931.  
PR 28-OCT-1999; 99US-0161931.  
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 20; DB 21; Length 38;  
Best Local Similarity 100.0%;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRAT 4  
DB 6 DRAT 11

RESULT 15  
AAM87857

ID AA87857 standard; Protein; 38 AA.  
XX AA87857;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
XX Human immune/haematopoietic antigen SEQ ID NO:15450.  
DE  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW Cytostatic; Gene therapy; vaccine; metastasis.  
XX  
OS Homo sapiens.  
XX  
XX WO200157182-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 17-JAN-2001; 2001NC-US01354.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.  
XX 19-MAR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0209467.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 14-JUL-2000; 2000US-0218436.  
XX 26-JUL-2000; 2000US-0220963.  
XX 26-JUL-2000; 2000US-0220964.  
XX 14-AUG-2000; 2000US-0224518.  
XX 14-AUG-2000; 2000US-0224519.  
XX 14-AUG-2000; 2000US-0225213.  
XX 14-AUG-2000; 2000US-0225214.  
XX 14-AUG-2000; 2000US-0225256.  
XX 14-AUG-2000; 2000US-0225256.  
XX 14-AUG-2000; 2000US-0225268.  
XX 14-AUG-2000; 2000US-0225270.  
XX 14-AUG-2000; 2000US-0225447.  
XX 14-AUG-2000; 2000US-0225757.  
XX 14-AUG-2000; 2000US-0225758.  
XX 14-AUG-2000; 2000US-0225759.  
XX 22-AUG-2000; 2000US-0225648.  
XX 22-AUG-2000; 2000US-0226868.  
XX 22-AUG-2000; 2000US-0227182.  
XX 23-AUG-2000; 2000US-0227009.  
XX 30-AUG-2000; 2000US-0228924.  
XX 01-SEP-2000; 2000US-0229287.  
XX 01-SEP-2000; 2000US-0229343.  
XX 01-SEP-2000; 2000US-0229344.  
XX 01-SEP-2000; 2000US-0229345.  
XX 05-SEP-2000; 2000US-0229509.  
XX 05-SEP-2000; 2000US-0229513.  
XX 06-SEP-2000; 2000US-0230437.  
XX 06-SEP-2000; 2000US-0230438.  
XX 08-SEP-2000; 2000US-0231242.  
XX 08-SEP-2000; 2000US-0231243.  
XX 08-SEP-2000; 2000US-0231413.  
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XX 08-SEP-2000; 2000US-0232080.  
XX 08-SEP-2000; 2000US-0232081.  
XX 12-SEP-2000; 2000US-0231968.  
XX 14-SEP-2000; 2000US-0232397.  
XX 14-SEP-2000; 2000US-0232398.  
XX 14-SEP-2000; 2000US-0232399.  
XX 14-SEP-2000; 2000US-0232400.  
XX 14-SEP-2000; 2000US-0232401.  
XX 14-SEP-2000; 2000US-0232402.  
XX 14-SEP-2000; 2000US-0233064.  
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XX 21-SEP-2000; 2000US-0234223.  
XX 21-SEP-2000; 2000US-0234274.  
XX 21-SEP-2000; 2000US-0234274.  
XX 25-SEP-2000; 2000US-0234997.  
XX 25-SEP-2000; 2000US-0234998.  
XX 27-SEP-2000; 2000US-0235834.  
XX 27-SEP-2000; 2000US-0235834.  
XX 27-SEP-2000; 2000US-0235836.  
XX 29-SEP-2000; 2000US-0236327.  
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XX 29-SEP-2000; 2000US-0236367.  
XX 29-SEP-2000; 2000US-0236368.  
XX 29-SEP-2000; 2000US-0236369.  
XX 29-SEP-2000; 2000US-0236370.  
XX 02-OCT-2000; 2000US-0237037.  
XX 02-OCT-2000; 2000US-0237038.  
XX 02-OCT-2000; 2000US-0237039.  
XX 02-OCT-2000; 2000US-0237040.  
XX 13-OCT-2000; 2000US-0239935.  
XX 13-OCT-2000; 2000US-0239937.  
XX 20-OCT-2000; 2000US-0240950.  
XX 20-OCT-2000; 2000US-0240950.  
XX 20-OCT-2000; 2000US-0241785.  
XX 20-OCT-2000; 2000US-0241786.  
XX 20-OCT-2000; 2000US-0241787.  
XX 20-OCT-2000; 2000US-0241808.  
XX 20-OCT-2000; 2000US-0241809.  
XX 20-OCT-2000; 2000US-0241809.  
XX 01-NOV-2000; 2000US-0244617.  
XX 08-NOV-2000; 2000US-0246476.  
XX 08-NOV-2000; 2000US-0246476.  
XX 08-NOV-2000; 2000US-0246477.  
XX 08-NOV-2000; 2000US-0246478.  
XX 08-NOV-2000; 2000US-0246523.  
XX 08-NOV-2000; 2000US-0246524.  
XX 08-NOV-2000; 2000US-0246525.  
XX 08-NOV-2000; 2000US-0246526.  
XX 08-NOV-2000; 2000US-0246527.  
XX 08-NOV-2000; 2000US-0246528.  
XX 08-NOV-2000; 2000US-0246532.  
XX 08-NOV-2000; 2000US-0246603.  
XX 08-NOV-2000; 2000US-0246610.  
XX 08-NOV-2000; 2000US-0246611.  
XX 08-NOV-2000; 2000US-0246613.  
XX 17-NOV-2000; 2000US-0249208.  
XX 17-NOV-2000; 2000US-0249209.  
XX 17-NOV-2000; 2000US-0249210.  
XX 17-NOV-2000; 2000US-0249211.  
XX 17-NOV-2000; 2000US-0249212.  
XX 17-NOV-2000; 2000US-0249213.  
XX 17-NOV-2000; 2000US-0249214.  
XX 17-NOV-2000; 2000US-0249215.  
XX 17-NOV-2000; 2000US-0249216.  
XX 17-NOV-2000; 2000US-0249217.  
XX 17-NOV-2000; 2000US-0249218.  
XX 17-NOV-2000; 2000US-0249244.  
XX 17-NOV-2000; 2000US-0249244.  
XX 17-NOV-2000; 2000US-0249264.  
XX 17-NOV-2000; 2000US-0249265.  
XX 17-NOV-2000; 2000US-0249269.  
XX 17-NOV-2000; 2000US-0249299.  
XX 17-NOV-2000; 2000US-0249300.  
XX 01-DEC-2000; 2000US-0250160.  
XX 01-DEC-2000; 2000US-0250391.  
XX 05-DEC-2000; 2000US-0251030.  
XX 05-DEC-2000; 2000US-0251988.

```

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-)* HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX N-PSDB; AAK60638.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
XX
XX Claim 11; SEQ ID NO 15450; 3071pp + Sequence Listing, English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of cancer. (I) polynucleotides may be used to express for
XX example, they may be used to treat the inappropriate (II) expression for
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent, ally
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK62169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 38 AA;

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Query March 100.0%; Score 20; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DRAT 4
DB 6 DRAT 9

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Search completed: May 6, 2003, 15:01:02
Job time : 19.2 secs

```



GenCore version 5.1.4.P5\_4578  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 14:58:45 ; Search time 24.85 seconds  
(without alignments)  
58.041 Million cell updates/sec

Title: US-09-851-422b-8

Perfect score: 39

Sequence: 1 VPHNESE 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:\*

1: sp.archaea:\*

2: sp.bacteria:\*

3: sp.fungi:\*

4: sp.invertebrate:\*

5: sp.invertebrate:\*

6: sp.mammal:\*

7: sp.mhc:\*

8: sp.organelle:\*

9: sp.phage:\*

10: sp.plant:\*

11: sp.potent:\*

12: sp.reptile:\*

13: sp.vertebrate:\*

14: sp.unclassified:\*

15: sp.virus:\*

16: sp.bacteriap:\*

17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	39	100.0	0	361	11	Q93416 archaea
2	36	92.3	315	10	Q93416	Q93416 archaea
3	36	92.3	315	10	Q93416	Q93416 archaea
4	36	92.3	315	10	Q93416	Q93416 archaea
5	35	89.7	1344	12	Q93928	Q93928 archaea
6	34	87.2	293	10	Q94071	Q94071 human herpe
7	34	87.2	293	10	Q94071	Q94071 archaea
8	34	87.2	293	10	Q94071	Q94071 archaea
9	34	87.2	293	10	Q94071	Q94071 archaea
10	33	84.6	381	16	Q94071	Q94071 archaea
11	33	84.6	510	5	Q97251	Q97251 plasmodesm
12	32	82.1	115	5	Q97251	Q97251 archaea
13	32	82.1	332	10	Q94587	Q94587 archaea
14	32	82.1	369	13	Q93345	Q93345 gallus gall
15	32	82.1	372	10	Q05699	Q05699 nicotiana t
16	32	82.1	1639	5	Q9VNF2	Q9VNF2 drosophila

17	32	82.1	1689	12	Q91W14	Q91W14 crimean-con
18	32	82.1	1689	12	Q92G30	Q92G30 crimean-con
19	32	82.1	1689	12	Q92G30	Q92G30 crimean-con
20	32	82.1	1689	12	Q92G30	Q92G30 crimean-con
21	31	79.5	249	10	Q9C557	Q9C557 arabidopsis
22	31	79.5	253	5	Q8T4L9	Q8T4L9 drosophila
23	31	79.5	272	5	Q9XW43	Q9XW43 caenorhabdi
24	31	79.5	316	16	Q8ZAG5	Q8ZAG5 yersinia pe
25	31	79.5	316	16	Q8ZAG5	Q8ZAG5 yersinia pe
26	31	79.5	374	5	Q91006	Q91006 caenorhabdi
27	31	79.5	374	5	Q91006	Q91006 caenorhabdi
28	31	79.5	487	5	Q9G522	Q9G522 ciona intes
29	31	79.5	534	5	Q9VSD7	Q9VSD7 drosophila
30	31	79.5	548	5	Q9XUC0	Q9XUC0 caenorhabdi
31	31	79.5	607	16	Q98AV5	Q98AV5 rhizobium 1
32	31	79.5	648	2	Q93FT6	Q93FT6 cowdria rum
33	31	79.5	782	17	Q97B85	Q97B85 thermoplas
34	31	79.5	1086	10	Q97B85	Q97B85 thermoplas
35	31	79.5	1086	10	Q97B85	Q97B85 thermoplas
36	31	79.5	1274	2	Q45563	Q45563 bacillus su
37	31	79.5	1391	3	Q8X0V7	Q8X0V7 neurospora
38	31	79.5	1467	10	Q9M033	Q9M033 arabidopsis
39	31	79.5	1474	5	Q8T4M0	Q8T4M0 drosophila
40	31	79.5	1503	5	Q8T4L8	Q8T4L8 drosophila
41	31	79.5	1509	5	Q9SP10	Q9SP10 drosophila
42	30	76.9	97	1	Q95522	Q95522 mus muscu
43	30	76.9	143	2	Q9Z5H0	Q9Z5H0 mycobacteri
44	30	76.9	143	2	Q9Z5H0	Q9Z5H0 mycobacteri
45	30	76.9	193	10	Q24284	Q24284 phoenix rec

## ALIGNMENTS

RESULT 1

ID Q9DCH4 PRELIMINARY; ERT; 361 AA.  
AC Q9DCH4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2002 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
E 01002 Q9DCH4 (1760aa) vs Q9DCH4 (361aa)  
E 01002 Q9DCH4 (1760aa) vs Q9DCH4 (361aa)  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN NCBI\_TaxID=10090;  
RX [1]

SEQUENCE FROM N.A. TISSUE-KIDNEY  
RC STRAIN=371/627, Tissue=KIDNEY  
RC STRAIN=371/627, Tissue=KIDNEY  
RA Kawai J, Shinagawa A, Shibata K, Yoshino M, Itoh M, Ishii Y,  
RA Arakawa T, Hara A, Fukunishi Y, Konno H, Adachi J, Fukuda S,  
RA Aizawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S, Yamanaka I,  
RA Saito T, Okazaki Y, Gojohori T, Bono H, Kasukawa T, Saito R,  
RA Kadota K, Matsuda H.A., Ashburner M, Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland P., Gissi C., King B., Kochwa H.,  
RA Klenk T., Krawchuk P., Smit A., Smith M., Smith M., Smith T.,  
RA Sakai K, Okido T, Furuno M, Aono H, Baldarelli R, Barsh G.G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Nishikawa K., Oka K., Oka K., Oka K., Oka K., Oka K., Oka K.,  
RA Sasaki H., Sato K., Sato K., Sato K., Sato K., Sato K., Sato K.,  
RA Sasaki H., Sato K., Sato K., Sato K., Sato K., Sato K., Sato K.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohntauki S.,  
RA Hayashizaki Y.  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
E EMBL; AK002778; BAB2352.1;  
DR MGD; MGI:191335; Eif3e5.

.

.

DT	01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DN	26S proteasome regulatory subunit.
GN	ATG39990.
OC	Arabidopsis thaliana (Mouse-ear cress).
OC	Bakaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	Eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC	NCHI_TaxID=3702;
OC	[1]
RP	SEQUENCE FROM N.A.
RA	Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA	Cheuk R., Chung K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA	Kawano T., Liang S.H., Maruyama M., Pham P.K., Sakai H.,
RA	Saito T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA	Ecker J., Theologis A., Davis R.W.;
RL	Submitted (NOV-2001) to the ENBL/GenBank/DBJ databases.
[2]	
RP	SEQUENCE FROM N.A.
RA	Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA	Ki-Chun C., Liu X., Lin S.X., Nakata M., Pham P.K., Sakai H.,
RA	Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA	Ecker J., Theologis A., Davis R.W.;
RL	Submitted (MAR-2002) to the ENBL/GenBank/DBJ databases.
DR	EMBL; AY062556; ALM32634.1; -
DR	EMBL; AY062558; AM33367.1; -
DR	InterPro; IPR000595; Mov34.
DR	RefSeq; NP_135800.3; Mov34.2.
DR	Problem; PD005425; Mov34.2; 1.
DR	SMART; SM00232; JAB_MENF.1.
SW	Proteasome.
KQ	SEQUENCE 293 AA; 31861 MW; 494CF29E8F67A7C CRC64;
Query Match	
Sequence Similarity	87.2%; Score 34; DB 10; Length 293;
Matches	6; Conservative 0; Missmatches 0; Indels 0; Gaps
OY	1 VPHNES 6
DB	
	74 VPHNES 79
RESULT 7	
ID	PRELIMINARY; PRT: 293 AA.
IC	AD 004202
AC	004202;
DT	01-JUL-1997 (TRENBLrel. 04, Created)
DT	01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE	26S proteasome regulatory subunit S12 ISOLGO (Pucative 26S proteasome
GN	TRENA1; ORFATG39990.
OC	Arabidopsis thaliana (Mouse-ear cress).
OC	Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC	NCHI_TaxID=3702;
OC	[1]
RP	SEQUENCE FROM N.A.
RA	Rounsfey S.D., Ketchum K.A., Lin X., Phillippe C.A., Brandon R.C.,
RA	Fuhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA	Venter J.C.;
RL	Submitted (MAR-1997) to the ENBL/GenBank/DBJ databases.
[2]	
RP	SEQUENCE FROM N.A.
RA	Rounsfey S.D., Ketchum H.-P., Richter-Cook N.J., Merrick W.C.,
RA	Hinnebusch G., Hershey J.W.B.,
RL	J. Biol. Chem. 0.0-0.13977.

SC	SEQUENCE	302 AA;	A046E087C0F08D84	CRC64;
	Query Match	87.2%;	Score 34; DB 3;	Length 302;
	Best Local Similarity	100.0%;	Pred. No. 33;	
	Matches	6;	Conservative	0; Mismatches
			0; Indels	0; Gaps
OY		1 VPINES 6		
Dd		70 VPHNES 75		
RESULT 9				
Q921F7	PRELIMINARY;	PTT;	377 AA.	
ID	Q921F7			
AC	Q921F7-2001 (TrEMBLrel. 19, Created)			
CD	Q921F7-2001 (TrEMBLrel. 19, Last annotation update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DD	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DN	Similar to farnesyltransferase, CAAX box, alpha.			
GN	FNTA.			
GC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Amniota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OB	NB1_043121.10390;			
RN	NB1_043121.10390;			
RE	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; BC012711; AH412711.1; -			
MD	MGD; MG1:104683; ENCA.			
PI	InterPro:IPR013278; PFTA.			
PR	PROSITE: PS00333; PFTS.			
PG	PROSITE: PS00304; PPTA; UNKNOWN_5.			
KW	Transferase.			
SC	SEQUENCE	377 AA;	44012 MW;	F3D8EF729D1D898C CRC64;
	Query Match	87.2%;	Score 34; DB 11;	Length 377;
	Best Local Similarity	100.0%;	Pred. No. 42;	
	Matches	6;	Conservative	0; Mismatches
			0; Indels	0; Gaps
OY		1 VPINES 6		
Dd		270 VPHNES 275		
RESULT 10				
U08UBO	PRELIMINARY;	PTT;	361 AA.	
ID	U08UBO			
AC	U08UBO			
CD	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DD	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DN	9-amino-7-oxononanoate synthase.			
DE	BIOF OR ATU3998 OR AGR_L1707.			
GC	Agrobacterium tumefaciens (strain C58 / ATCC 33970).			
OC	Proteobacteria; Gammaproteobacteria; Rhizobiaceae group;			
OB	Rhizobiaceae; Rhizobium.			
RN	NCBI_TaxId=176259;			
RE	[1]			
RA	SEQUENCE FROM N.A.			
RL	MEDLINE=21609550; PubMed=11743193;			
DR	Wood D.W., Stubbai J.C., Kaul R.K., Monks D.E., Kitajima J.P.,			
MD	Kurikawa Y., Zhou L., Chen J., Wood K.A., Blevins D.J., Moo L.,			
PI	Okura Y., Paulsen I.T., Ellis J.A., Blevins D.J.,			
PR	Chapman P., Glendinning J.F., Deatherage G., Gillet W., Grant C.,			
PG	Kucyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,			
KN	Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,			
RA	Zhang S., Too H., Tao Y., Biddle P., Jung M., Krupan W., Perry M.,			
RR	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,			
RR	Chumley F., Tingey S.V., Tomb J.-P., Gordon M.V., Olson M.V.,			
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens C58."			

```

RL Science 294:2317-2323(2001).
RM SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Akenchuk O., Mullin L.,
RA Houtmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA "Gene" sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.
RL Science 294:2323-2328(2001).
DR EMBL; AF009331; AAL4800.1; -.
DR EMBL; AF008283; AAK89477.1; -.
KW Complete proteome.
SQ SEQUENCE 381 AA; 39773 MW; 952964CEB3EC3FB CRC64;

Query Match 84.6%; Score 33; DB 5; Length 381;
Best Local Similarity 85.3%; Pred. No. 69;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1. VPHNESE 7
DB 140 VPHNEVE 146

RESULT 11
ID 097251 PRELIMINARY; PRT; 510 AA.
AC DT 01-MAY-1999 (TREMBLrel. 10, Created)
AD 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Putative homolog of human E51 protein.
DE PFC0305W, MAL3P2 30.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=3D7; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Felwell T.,
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jaesal B., Kyes S., McLean J., Moulie S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Whithead S., Skilton J., Squares R., Squares S., Sutton J.E.,
RA "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum".
RL Nature 400:532-538(1999).
DR EMBL; AL034558; CAB39017.1; -.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR004953; EB1.
DR PRSITE: PS027185.1; EB1.
DR PRSITE: PS027185.1; EB1.
SQ SEQUENCE 510 AA; 59544 MW; 2980BDG20359325B CRC64;

Query Match 84.6%; Score 33; DB 5; Length 510;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNES 6
DB 489 IPINES 494

RESULT 12
QSV553
ID QSV553 PRELIMINARY; PRT; 115 AA.
AC QSV153;

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT CG1248.20 (TREMBLrel. 20, Last annotation update)
GN Drosophila melanogaster (Fruit fly).
GN CG1195 OR CG12482.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pharyngota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridiodes; Drosophilidae; Drosophila.
NCBI_taxid=7227;
XP 1. VPHNESE 7
RP 140 VPHNEVE 146
RX STRAIN=BERKELEY.
RC MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.O., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.C., Maniatis T., Yeaman S., Zhang Q., Chuvpilo I.,
RA Burtis K.C., Rhee V., H.C. Rhee, P.G. Chuvpilo, M. Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Niklos G.L.G.,
RA Abiril J.J., Abayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtova D., Botchan M.R., Bouck J., Brokstein P., Brattler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Ciesla A., Dalke C., Davenport L.B., Davies P.,
RA Degen J.B., Delcher A.L., Desmetz C., Drenth J., Drenth S.W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foelel K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeguan C.,
RA Jaitani B., Katoun P., Karpman G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jia H., Jia J., Jia L., Jia S., Jia T., Jia Y., Jia X.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Jiang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.W.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Part V., Reese M.G.,
RA Paoletti M., Paoletti M., Paoletti M., Paoletti M., Paoletti M.,
RA Shie B.C., Siden-Kimone I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Nassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong X., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA "The complete nucleotide sequence of Drosophila melanogaster".
RL Science 287:2185-2195(2000).
DR EMBL; AF003495; AAF48352.1; -.
DR FlyBase; FBgn0030546; CG11595.
SQ SEQUENCE 115 AA; 13640 MW; CEE29A8CBF402AB CRC64;

Query Match 92.1%; Score 32; DB 5; Length 115;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7
DB 56 VPHNEKD 62

RESULT 13
CD 5657
AC 5657 PRELIMINARY; PRT; 332 AA.
ID Q9LEST;
AD Q9LEST;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Hypothetical 37.1 kDa protein.

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[illegible]





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CC      THE BETA SUBUNIT BINDS THE PEPTIDE SUBSTRATE.
CC      -1- SIMILARITY: BELONGS TO THE PROTEIN FARNESYLTRANSFERASE ALPHA SUBUNIT
CC      -1- FAMILY.
CC      -1- SIMILARITY: CONTAINS 5 PFTA REPEATS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL; D49744; BAA08578.1;
CC      HSSP; Q04631; 1FT1.
CC      DR      MG1;104683; PFTA.
CC      DR      Pfam; PF01239; PFTA; 5.
CC      DR      PROSITE; PS00304; PPTA; 5.
CC      KW      Transferase; Prenyltransferase; Repeat.
CC      KW      DOMAIN 22 30 POLY-PRO.
CC      FT      REPEAT 115 148 PFTA 1.
CC      FT      REPEAT 150 183 PFTA 2.
CC      FT      REPEAT 184 217 PFTA 3.
CC      FT      REPEAT 218 251 PFTA 4.
CC      FT      REPEAT 258 291 PFTA 5.
CC      SQ      SEQUENCE 377 AA; 44013 MW; F3D608989F3D66 CRC64;

Query Match      87.2%; Score 34; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VPINES 6
DB 270 VPINES 275

STANDARD; PRT; 377 AA.

ID PFTA RAT
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase alpha subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase alpha subunit) (RAS proteins prenyltransferase
DE alpha) (Frase-alpha).
DE PFTA.
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
DE NCBI_TaxID=10116;
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 RA Alengraber A., Beck R.S., Folschroder M., Spudich J.L., Jung K.-H.,  
 RA Ebbard H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.,  
 RA "Genome sequence of *Halobacterium* species NRC-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 RL [2]  
 RL SEQUENCE OF 1-23.  
 RP SPECIES-Halobacterium, STRAIN-DEM 3754;  
 CC SPECIES-Halobacterium, STRAIN-DEM 3754;  
 CC Mcdougall J. Mitman-Liebold A.  
 RA "Comparative analysis of the protein components from 5S rRNA protein  
 RT complexes of halophilic archaeobacteria.";  
 RT Eur. J. Biochem. 221:779-785(1994).  
 CC -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC DB |D33000702|Q61955:1| -  
 CC PRT: 133 VPNNRS 6  
 DR InterPro: IPR001149; Ribosomal L18p.  
 DR Pfam: PF00861; Ribosomal L18p; 1.  
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 CC RESULT 9  
 CC HM36 CAEEL STANDARD; PRT: 254 AA.  
 CC AC Q93352;  
 CC DT 15-JUL-1998 (Rel. 36, Created)  
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 CC CE51-36 OR Protein celh-36.  
 CC Caenorhabditis elegans.  
 CC OS Caenorhabditis elegans.  
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 CC OC Rhabditidae; Plectoderinae; Caenorhabditidae.  
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 CC RC STRAIN=riscol N2;  
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 CC (2)  
 CC CONCEPTUAL TRANSLATION.  
 CC RA Spring J.;  
 CC RA Unpublished observations (JUN-1999).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
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 CC EMBL: Z81046; CAB02821.1; AUT\_SEQ.  
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 DR WormPep: C3782.4; CR08623.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; Homeobox; 1.  
 DR GDOM: G00000101; Homeobox; 1.  
 DR SMART: SM00010; Homeobox; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS00071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
 FT DNA BIND 55 111 HOMEBOX.  
 FT DOMAIN 171 182 POLY-GLN.  
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 CC 133 PNESEK 138  
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 CC RESULT 10  
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 CC AC P27841;  
 CC DT 01-AUG-1992 (Rel. 23, Created)  
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC KW Enterobacteriaceae; Proteobacteria; Proteobacteria; Proteobacteria.  
 CC CORA OR B3816 OR 25533 OR ECS4746.  
 CC Escherichia coli.  
 CC OS Escherichia coli O157:H7.  
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 CC OC Escherichia.  
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 CC RX Sequence from N.A.  
 CC MEDLINE=93100795; PubMed=8314774;  
 CC Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.;  
 CC "Sequence and topology of the *CorA* magnesium transport systems of  
 CC *Salmonella typhimurium* and *Escherichia coli*. Identification of a new  
 CC class of transport protein.";  
 CC RL J. Biol. Chem. 268:14071-14080(1993).  
 CC RC Sequence from N.A.  
 CC RC STRAIN=K12;  
 CC RC Ohmori H.;  
 CC RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
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 CC SEQUENCE FROM N.A.  
 CC RC STRAIN=K12 / MG1655;  
 CC RC MEDLINE=933795; PubMed=8346018.  
 CC RX "Analysis of the *Escherichia coli* genome. III. DNA sequence of the  
 CC region from 87.2 to 89.2 minutes.";  
 CC RL Science 257:771-778(1992).  
 CC (4)  
 CC REVISIONS.  
 CC RC STRAIN=K12 / MG1655;  
 CC RC MEDLINE=933795; PubMed=8346018.  
 CC RX "Analysis of the *Escherichia coli* genome. III. DNA sequence of the  
 CC region from 87.2 to 89.2 minutes.";  
 CC RL Nucleic Acids Res. 21:3391-3398(1993).  
 CC (5)  
 CC SEQUENCE FROM N.A.  
 CC RC STRAIN=O157:H7 / EDL933 / ATCC 700929;





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Query Match
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PHNSES 7
DB 803 PHNSES 808

RESULT 14
CMA CYCA
CMA CYCA STANDARD; PRT; 278 AA.
CMA CYCA
CMA CYCA
16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast envelope membrane protein.
DE CMA OR YCF10 OR YCF56.
OS Cyanidium caldarium.
OC Chloroplast.
OC Rhodophyta; Rhodophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OC NCB1_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-1;
RC MEDLINE=20496559; PubMed11040290;
RC CMA CYCA
RC CMA CYCA
RT "The structure and gene repertoire of an ancient red algal plastid genome."
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: May be involved in proton extrusion. Indirectly promotes efficient inorganic carbon uptake into chloroplasts (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CMA FAMILY.
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CC EMBL; AF022186; AAF12995.1; -
CC InterPro; IPR004282; CMA.
CC Pfam; PF03040; CMA; 1.
CC TRANSMEM 155 175 POTENTIAL.
CC TRANSMEM 203 223 POTENTIAL.
CC TRANSMEM 239 259 POTENTIAL.
CC SEQUENCE 278 AA; 32355 MW; 88B1050D7836102E CRC64;
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Best Local Similarity 76.9%; Score 30; DB 1; Length 278;
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OY 2 PHNSES 7
DB 37 PHSESE 42

RESULT 15
CMA CYCA
CMA CYCA STANDARD; PRT; 315 AA.
CMA CYCA
CMA CYCA
16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Chloroplast envelope membrane protein.
DE CMA OR YCF10 OR YCF56.
OS Cyanidium caldarium.
OC Chloroplast.
OC Rhodophyta; Rhodophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OC NCB1_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-1;
RC MEDLINE=20496559; PubMed11040290;
RC CMA CYCA
RC CMA CYCA
RT "The structure and gene repertoire of an ancient red algal plastid genome."
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: May be involved in proton extrusion. Indirectly promotes efficient inorganic carbon uptake into chloroplasts (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CMA FAMILY.
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CC EMBL; AF022186; AAF12995.1; -
CC InterPro; IPR004282; CMA.
CC Pfam; PF03040; CMA; 1.
CC TRANSMEM 155 175 POTENTIAL.
CC TRANSMEM 203 223 POTENTIAL.
CC TRANSMEM 239 259 POTENTIAL.
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PHNES 6
DB 227 PHNES 231

Search completed: May 6, 2003, 15:01:31
Job time : 9 secs

Magnesium and cobalt transport protein cora.
CORA OR HI1035.
OC Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OC NCB1_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RC MEDLINE=95350630; PubMed7542800;
RC Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kieley A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McEwen H.R., Skrzypek M.S., Olsen G.J., Peterson J., Smith T.A., Wilson R.A., Kohnen M., Shetty B., Fitzhugh W., Glendon C., Kelley T., Weller J.F., Phillips C.A., Spriggs T., Hadjilov E., Cotton M.D., Utterback T.R., Hanna M.C., Spriggs T., Hadjilov E., Cotton M.D., Utterback T.R., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
RC Science 269:496-512(1995).
CC -!- FUNCTION: PLAYS A ROLE IN THE TRANSPORT OF MAGNESIUM AND COBALT IONS (BY SIMILARITY).
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CC EMBL; U32784; AAC22595.1; -
CC TIGR; HI1035; -
CC InterPro; IPR004282; CORA_transp.
CC Pfam; PF01544; CORA; 1.
CC TRANSMEM 289 309 POTENTIAL.
CC SEQUENCE 315 AA; 36593 MW; D44EDA284CC68DCC CRC64;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PHNES 6
DB 227 PHNES 231

Search completed: May 6, 2003, 15:01:31
Job time : 9 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 6, 2003, 14:59:05 ; Search time 12.25 seconds  
(without alignments)  
54,934 Million cell updates/sec

Title: US-09-851-422B-8  
Perfect score: 39  
Sequence: 1 VPHNSE 7

Scoring table: BLOSSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum March 0s  
Maximum March 100s  
Listing first 45 summaries

Database: PIR 73:\*

1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	36	92.3	320	2 F96570	unknown protein, 8
2	35	89.7	1345	2 T41960	major capsid prote
3	34	87.2	293	2 H84823	26S proteasome reg
4	34	87.2	302	2 T40490	probable 26S prote
5	34	87.2	340	2 T41013	protein farnesyltr
6	34	87.2	377	2 T41625	protein farnesyltr
7	34	87.2	377	2 T41625	protein farnesyltr
8	34	87.2	379	2 A47659	farnesyl-protein t
9	33	84.6	381	2 A96238	biof protein (AF31
10	33	84.6	381	2 AB3048	8-amino-7-oxonon
11	32	82.1	332	2 T51269	hypothetical prote
12	32	82.1	372	2 S17715	transcription acti
13	32	82.1	488	2 T37923	hypothetical prote
14	31	79.5	183	2 C84323	50S ribosomal ph
15	31	79.5	183	2 C84323	50S ribosomal ph
16	31	79.5	249	2 D96691	hypothetical prote
17	31	79.5	257	2 T19809	hypothetical prote
18	31	79.5	272	2 T26235	hypothetical prote
19	31	79.5	288	2 T48753	conserved hypotet
20	31	79.5	316	2 A47157	magnesium transpor
21	31	79.5	316	2 A50467	magnesium transpor
22	31	79.5	316	2 A50467	magnesium and coba
23	31	79.5	316	2 AF0918	magnesium and coba
24	31	79.5	316	2 B86068	Mg2+ transport, sy
25	31	79.5	316	2 E91222	Mg2+ transport, sy
26	31	79.5	316	2 C81720	conserved hypotet
27	31	79.5	374	2 T15895	hypothetical prote
28	31	79.5	382	2 T25538	hypothetical prote
29	31	79.5	348	2 T23424	hypothetical prote

hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
gamma4-crystallin  
hypothetical prote  
lysophospholipase  
magnesium transpor  
hypothetical prote  
conserved hypotet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
thyrroxine-binding  
synaptotagmin P65  
hypothetical prote

#### ALIGNMENTS

##### RESULT 1

F96570  
unknown protein, 80333-82175 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzall  
K.; M.; Salazar, T.; Row, S.; Sakano, T.; Sakano, T.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; W.D.; Y.G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MUID:21016719; PMID:11130712  
A:Accession: F96570  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 320 <870>  
A:Codon preferences: GB:AB005173; MID:G6862953; PIDN:AAF30341.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F14G24.20  
A:Map position: 1  
C:Superfamily: probable membrane protein YOLO77c

Query Match 92.3% Score 36; DB 2; Length 320;  
Best local Similarity 85.4%; Pred. No. 6.8;  
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QV 1 VPHNSE 7

|||||  
DB 222 VPHNSED 228

##### RESULT 2

T41960  
major capsid protein - human herpesvirus 7 (strain J1)  
C:Species: human herpesvirus 7  
A:Variety: strain J1  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
C:Accession: T41960  
R:Ritchie, J.; the EMBL Data Library, December 1995  
A:Description: Determination and analysis of the complete nucleotide sequence of human  
A:Reference number: 222022  
A:Accession: T41960  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1345 <NIC>  
A:Cross-references: EMBL:U043400; PIDN:AMC54720.1

A:Experimental source: strain J1

C:Genetics:

C:Note: U57

C:Superfamily: varicella-zoster virus major capsid protein

Query Match 89.7%; Score 35; DB 2; Length 1345;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHNESE 7

DB 1181 PHNESE 1186

RESULT 3

H84823

265 proteasome regulatory subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

A:Accession: H84823

A:Residues: 1-293 <STO>

A:Status: preliminary

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: H84420; MUID:20083487; PMID:10617197

A:Cross-references: GB:A8002093; NID:g2088652; PIDN:AAB95284.1; GSPDB:GN00139

A:Gene: At2g39990

A:Map position: 2

Query Match 87.2%; Score 34; DB 2; Length 293;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPINES 6

DB 74 VPINES 79

RESULT 4

T40490

probable 26S proteasome regulatory subunit - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

A:Accession: T40490

A:Residues: 1-302 <WOO>

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Cross-references: EMBL:AL021730; PIDN:CAA16893.1; GSPDB:GN00067; SPDB:SPBC4C3.07

A:Gene: SPDB:SPBC4C3.07

A:Map position: 2

C:Superfamily: mov-34 protein

Query Match 87.2%; Score 34; DB 2; Length 302;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPINES 6

DB 70 VPINES 75

RESULT 5

A41013

protein farnesyltransferase (EC 2.5.1.-) alpha chain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 6-Oct-1992 #sequence\_revision 16-Oct-1992 #text\_change 28-May-1993

A:Accession: A41013

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005

A:Accession: A41013

A:Molecule type: mRNA

A:Residues: 1-340 <KDS>

A:Status: preliminary

A:Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro

A:Reference number: A41013; MUID:92011656; PMID:1918005



C:Comment: This protein attaches farnesyl residues to a cysteine near the carboxyl termi  
C:Keywords: heterodimer; transferase

Query Match 87.3%; Score 34; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VPHNES 6  
|||||  
DB 270 VPHNES 275

## RESULT 8

AB3048  
farnesyl-protein transferase alpha chain - human  
N:Alternate names: CAAX farnesyltransferase alpha chain; FPPase alpha chain; prenyl-pro  
C:Species: Homo sapiens (man)  
C:Date: 22-Oct-2001 #sequence\_revision 10-May-1996 #text\_change 21-Jul-2000  
C:Accession: A47659; A49274  
R:Wood, D.W.; Gettel, W.; Grant, C.; Quentmer, D.; Kutyavin, T.; Levy, R.; Li, M.; McElie  
R:Andres, D.A.; Milatovich, A.; Ozelik, T.; Wenzlau, J.M.; Brown, M.S.; Goldstein, J.L.  
Genomics 18, 105-112, 1993  
A:Title: cDNA cloning of the two subunits of human CAAX farnesyltransferase and chromoso  
A:Reference number: A47659; MUID:94102736; PMID:8276393  
A:Accession: A47659  
A:Status: preliminary  
A:Gene: 1179 <AND>  
A:Residues: 1-179 <AND>  
A:Cross-references: GB:I0413; NID:q38755; PID:AA86285.1; PID:q38756  
R:Omet, C.A.; Kral, A.M.; Diehl, R.E.; Prendergast, G.C.; Powers, S.; Allen, C.M.; Gibbs  
Biochemistry 32, 5167-5176, 1993  
A:Title: Characterization of recombinant human farnesyl-protein transferase: cloning, ex  
A:Reference number: A49274; MUID:93264431; PMID:8494894  
A:Accession: A49274  
A:Status: preliminary  
A:Gene: type: mRNA; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-379 <OME>  
A:Experimental source: placenta  
A:Note: sequence extracted from NCBI backbone (NCBIP:132814)  
C:Genetics:  
A:Gene: GDB:FNTA  
A:Cross-references: GDB:138173; OMIM:134635  
A:Molecule type: cDNA  
A:Map position: 932-8611  
C:Keywords: heterodimer

Query Match 87.3%; Score 34; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNES 6  
|||||  
DB 270 VPHNES 275

## RESULT 9

AB5238  
BicP protein (AF111739) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 11-Jan-2002  
C:Accession: A96238  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Laggas, C.; Markalz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; PMID:11743194  
A:Accession: A97359  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-381 <KUR>  
A:Cross-references: GB:AE007870; PID:AAK89427.1; PID:g15159286; GSPDB:GN00170  
C:Genetics:  
A:Gene: AGT\_L1707  
A:Map position: linear chromosome  
C:Superfamily: 5-aminolevulinate synthase; glycine C-acetyltransferase homology

Query Match 84.6%; Score 33; DB 2; Length 381;  
Best Local Similarity 85.7%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 140 VPHNEVE 146

## RESULT 11

TS1269  
hypothetical protein TM16\_140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
R:Accession: T51269  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: 225346  
A:Accession: T51269  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332 <BEN>  
A:Cross-references: EMBL:AL309921  
A:Experimental source: cultivar Columbia; BAC clone TM16  
C:Genetics:  
A:Map position: 3  
A:Introns: 150/1  
A:Note: TM16\_140

Query Match 84.6%; Score 33; DB 2; Length 381;  
Best Local Similarity 85.7%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 140 VPHNEVE 146

## RESULT 11

TS1269  
hypothetical protein TM16\_140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
R:Accession: T51269  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: 225346  
A:Accession: T51269  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332 <BEN>  
A:Cross-references: EMBL:AL309921  
A:Experimental source: cultivar Columbia; BAC clone TM16  
C:Genetics:  
A:Map position: 3  
A:Introns: 150/1  
A:Note: TM16\_140

Query Match 82.1%; Score 32; DB 2; Length 332;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 88 LPHNEGE 94

## RESULT 11

TS1269  
hypothetical protein TM16\_140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
R:Accession: T51269  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: 225346  
A:Accession: T51269  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332 <BEN>  
A:Cross-references: EMBL:AL309921  
A:Experimental source: cultivar Columbia; BAC clone TM16  
C:Genetics:  
A:Map position: 3  
A:Introns: 150/1  
A:Note: TM16\_140

Query Match 82.1%; Score 32; DB 2; Length 332;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 88 LPHNEGE 94

## RESULT 11

TS1269  
hypothetical protein TM16\_140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
R:Accession: T51269  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: 225346  
A:Accession: T51269  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332 <BEN>  
A:Cross-references: EMBL:AL309921  
A:Experimental source: cultivar Columbia; BAC clone TM16  
C:Genetics:  
A:Map position: 3  
A:Introns: 150/1  
A:Note: TM16\_140

Query Match 82.1%; Score 32; DB 2; Length 332;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 88 LPHNEGE 94

## RESULT 11

TS1269  
hypothetical protein TM16\_140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
R:Accession: T51269  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: 225346  
A:Accession: T51269  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332 <BEN>  
A:Cross-references: EMBL:AL309921  
A:Experimental source: cultivar Columbia; BAC clone TM16  
C:Genetics:  
A:Map position: 3  
A:Introns: 150/1  
A:Note: TM16\_140

Query Match 82.1%; Score 32; DB 2; Length 332;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPHNESE 7  
|||||  
DB 88 LPHNEGE 94

```

RESULT 12
SI7715
transcription activator TGA1a - tobacco
C:Species: Nicotiana sp. (tobacco)
C>Date: 03-Mar-1999 #sequence_revision 19-Mar-1997 #text_change 16-Dec-1998
C:Reference number: SI7715
R:Promoter: H.; Katagiri, P.; Chua, N.H.
Mol. Gen. Genet. 229, 181-188, 1991
A:Title: The tobacco transcription activator TGA1a binds to a sequence in the 5' upstream
A:Reference number: SI7715; MUID:92017650; PMID:1921969
A:Accession: SI7715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <CON>
A:Cross-references: GB:AK7377; EPRO
C:Note: he sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 355-Glu
C:Superfamily: fos/jun DNA-binding domain homology
F:81-124/Domain: fos/jun DNA-binding domain homology <FUD>

Query Match      82.1%; Score 32; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHNESE 7
DB 60 PHNETE 65

RESULT 13
T37923
hypothetical protein SPAC18G6.10 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37923
R:Conor, R.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, December 1995
A:Reference number: T37923; Z21754
A:Accession: T37923
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-688 <CON>
A:Cross-references: EMBL:Z68198; PIDN:CAA92388.1; GSPDB:GN00066; SFDB:SPAC18G6.10
A:Experimental source: strain 972h-; cosmid c1866
C:Genet:GSPDB:SPAC18G6.10
A:Map position: 1

Query Match      82.1%; Score 32; DB 2; Length 688;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHNESE 7
DB 97 PHNETE 102

RESULT 14
D97132
uncharacterized phage related protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 03-Mar-1999 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97132
R:Moelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A95900; MUID:21359325; PMID:21359325
A:Accession: A95900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1819 <KUR>
A:Cross-references: GB:AK9001437; PIDN:AK79847.1; PID:gi5024862; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:

```

```

A:Gene: CAC1883

Query Match      82.1%; Score 32; DB 2; Length 1819;
Best Local Similarity 87.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNESE 7
DB 1289 IPHNSQ 1295

RESULT 15
S6222
ribosomal protein l2ap [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84323
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lesky,
; Leitthauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddock, D.G.; Jahl,
Jung, K.H.; Alam, M.; Freitas, T.; 12176-12181, 2000
A:Title: Genomic sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: G84323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-183 <STO>
A:Cross-references: GB:AE004437; NID:gi0581178; PIDN:AAG19955.1; GSPDB:GN00138
C:Genet:GSPDB:G84323
A:Map position: 18p

Query Match      79.5%; Score 31; DB 2; Length 183;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNESE 6
DB 130 VPHNSD 135

Search completed: May 6, 2003, 15:03:31
Job time : 14.25 secs

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GenCore version 5.1.4\_P5\_4578  
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 15:01:10 | Search time 14 Seconds  
(without alignments)  
43.143 Million cell updates/sec

Title: US-09-851-422b-8

Perfect score: 39

Sequence: 1 VPHNSE 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW PUB. pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW PUB. pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW PUB. pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US06\_NEW PUB. pep.\*  
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14: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB. pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	39	100.0	357	9	US-09-809-391-755
2	34	87.2	394	10	US-09-925-302-722
3	34	87.2	394	10	US-09-925-302-722
4	31	79.5	316	8	US-08-945-749-5
5	31	79.5	648	9	US-10-081-051-22
6	30	76.9	315	8	US-08-945-749-6
7	30	76.9	419	9	US-10-182-263-1
8	30	76.9	419	9	US-10-182-263-3
9	30	76.9	419	9	US-10-182-263-4
10	30	76.9	419	9	US-10-182-263-5
11	30	76.9	419	9	US-10-182-263-6
12	30	76.9	419	9	US-09-978-937-6
13	30	76.9	423	9	US-09-866-570A-56
14	30	76.9	448	9	US-09-866-570A-56
15	30	76.9	448	10	US-09-866-572A-56
16	30	76.9	461	9	US-10-182-263-2
17	30	76.9	461	9	US-09-978-917A-2
18	30	76.9	491	9	US-10-029-180-106
19	30	76.9	610	10	US-09-764-891-4164

Sequence 48731, A  
Sequence 16570, A  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 50, Appl  
Sequence 50, Appl  
Sequence 430, Appl  
Sequence 938, Appl  
Sequence 16, Appl  
Sequence 19, Appl  
Sequence 2, Appl  
Sequence 78, Appl  
Sequence 979, Appl  
Sequence 1372, Ap  
Sequence 1318, Ap  
Sequence 6579, Ap  
Sequence 6579, Ap  
Sequence 71, Appl  
Sequence 4982, Ap  
Sequence 10771, A  
Sequence 176, Appl  
Sequence 2, Appl  
Sequence 32, Appl  
Sequence 4164, Ap

20 29 74.4 29 10 US-09-864-761-48731  
21 29 74.4 29 10 US-09-864-761-48731  
22 29 74.4 29 10 US-09-864-761-48731  
23 29 74.4 302 10 US-09-866-572A-10  
24 29 74.4 443 9 US-09-866-570A-50  
25 29 74.4 443 10 US-09-866-572A-50  
26 29 74.4 438 9 US-09-893-919A-33  
27 29 74.4 650 10 US-09-801-368-430  
28 29 74.4 890 9 US-10-101-464A-938  
29 29 74.4 1372 9 US-09-925-302-722  
30 29 74.4 1134 9 US-09-836-392-16  
31 29 74.4 1173 9 US-10-135-322-19  
32 29 74.4 1176 9 US-09-918-508-2  
33 29 74.4 1237 10 US-09-862-027-78  
34 29 74.4 1270 9 US-10-101-464A-979  
35 28 71.8 157 10 US-09-925-301-1372  
36 28 71.8 157 10 US-09-925-301-1372  
37 28 71.8 157 10 US-09-925-301-1372  
38 28 71.8 400 9 US-09-738-626-6579  
39 28 71.8 400 9 US-10-101-464A-71  
40 28 71.8 804 10 US-09-815-242-4982  
41 28 71.8 820 10 US-09-815-242-10771  
42 28 71.8 1172 9 US-08-712-363-176  
43 28 71.8 1620 10 US-09-827-949-2  
44 28 69.2 42 10 US-09-836-392-16  
45 27 69.2 43 9 US-09-764-891-4164

## ALIGNMENTS

### RESULT 1

US-09-809-391-755  
US-09-809-391-755 Application US/09809391  
Publication No. US20030049618A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 18c Human Secreted proteins  
FILE REFERENCE: P2002P2  
CURRENT APPLICATION NUMBER: US/09/809,391  
CURRENT FILING DATE: 2001-03-16  
PRIORITY DATE: 2001-03-16  
PRIORITY NO.: 09/000,000  
NUMBER OF SEQ. IDS: 761  
SOFTWARE: PatentIn Ver. 2.0  
SBO ID NO 755  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE: SITS  
LOCATION: (68)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-809-391-755

Query Match 100.0%; Score 39; DB 9; Length 357;  
Best local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNSE 7

DB 137 VPHNSE 143

### RESULT 2

US-09-925-302-722  
US-09-925-302-722 Application US/09925302  
Publication No. US20020044941A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10



; EARLIER FILING DATE: 1995-05-01  
 ; SEQ ID NOS: 16  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 6  
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 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Hin  
 US-08-945-749-6

Query Match 76.9%; Score 30; DB 8; Length 315;  
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QY 2 PHNES 6  
 DB 227 PHNES 231

RESULT 7  
 US-10-182-263-1  
 ; Sequence 1, Application US/10182263  
 ; Publication No. US20030022354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerlitz, Bruce E  
 ; APPLICANT: Jones, Bryan W  
 ; APPLICANT: Grinnell, Brian W  
 ; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
 ; FILE REFERENCE: X-13611  
 ; CURRENT APPLICATION NUMBER: US/10/182,263  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 60/181948  
 ; PRIOR FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: 60/189199  
 ; PRIOR FILING DATE: 2000-03-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 419  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-182-263-1

Query Match 76.9%; Score 30; DB 9; Length 419;  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPNE 5  
 DB 326 VPNE 330

RESULT 8  
 US-10-182-263-3  
 ; Sequence 3, Application US/10182263  
 ; Publication No. US20030022354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerlitz, Bruce E  
 ; APPLICANT: Jones, Bryan W  
 ; APPLICANT: Grinnell, Brian W  
 ; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
 ; FILE REFERENCE: X-13611  
 ; CURRENT APPLICATION NUMBER: US/10/182,263  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 60/181948  
 ; PRIOR FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: 60/189199  
 ; PRIOR FILING DATE: 2000-03-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 419

; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-182-263-3

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QY 1 VPNE 5  
 DB 326 VPNE 330

RESULT 9  
 US-10-182-263-4  
 ; Sequence 4, Application US/10182263  
 ; Publication No. US20030022354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerlitz, Bruce E  
 ; APPLICANT: Jones, Bryan W  
 ; APPLICANT: Grinnell, Brian W  
 ; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
 ; FILE REFERENCE: X-13611  
 ; CURRENT APPLICATION NUMBER: US/10/182,263  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 60/181948  
 ; PRIOR FILING DATE: 2002-02-11  
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 US-10-182-263-4

Query Match 76.9%; Score 30; DB 9; Length 419;  
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QY 1 VPNE 5  
 DB 326 VPNE 330

RESULT 10  
 US-10-182-263-5  
 ; Sequence 5, Application US/10182263  
 ; Publication No. US20030022354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerlitz, Bruce E  
 ; APPLICANT: Jones, Bryan W  
 ; APPLICANT: Grinnell, Brian W  
 ; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
 ; FILE REFERENCE: X-13611  
 ; CURRENT APPLICATION NUMBER: US/10/182,263  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 60/181948  
 ; PRIOR FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: 60/189199  
 ; PRIOR FILING DATE: 2000-03-14  
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 ; ORGANISM: Homo sapiens  
 US-10-182-263-5

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; PRIOR FILING DATE: 1999-12-07  
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; ORGANISM: Taxus cuspidata  
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Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPNNES 6  
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Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: May 6, 2003, 14:59:30 | Search time 11.2 Seconds  
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Title: US-09-851-422b-8

Perfect score: 39

Sequence: 1 VPRNESE 7

Scoring table: BLOSUM62

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database : Issued Patents AA:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	357	4	US-09-149-476-755
2	34	87.2	377	1	US-07-863-169A-1
3	34	87.2	377	2	US-08-429-964-1
4	34	87.2	377	3	US-08-429-964-1
5	34	87.2	377	5	US-07-863-169A-1
6	34	87.2	379	1	US-07-863-169A-1
7	34	87.2	379	2	US-08-424-268-8
8	34	87.2	379	2	US-08-429-964-5
9	34	87.2	379	3	US-07-835-087-5
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13	34	87.2	379	5	US-07-835-087-5
14	31	79.5	146	1	US-08-173-510B-88
15	31	79.5	146	1	US-08-458-218-86
16	31	79.5	146	2	US-08-450-497-88
17	30	76.9	250	4	US-08-944-483-51
18	30	76.9	261	6	US-07-863-169A-1
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21	30	76.9	261	6	US-07-863-169A-1
22	30	76.9	262	1	US-07-720-189-1
23	30	76.9	409	4	US-09-065-872-2
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26	30	76.9	410	4	US-09-667-570A-1
27	30	76.9	410	1	US-08-295-511-1

Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 56, Appli  
Sequence 2, Appli  
Sequence 4, Appli  
Patent No. 5270178  
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Patent No. 5270178  
Patent No. 5270178  
Patent No. 5270178  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 6, Appli

#### ALIGNMENTS

RESULT 1  
US-09-149-476-755  
; Sequence 755, Application US/09149476  
; Title: 186 Human Secreted Proteins  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted Proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; PRIORITY DATE: 1998-09-08 / US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
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; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
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; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
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; EARLIER APPLICATION NUMBER: 60/047,597  
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; EARLIER APPLICATION NUMBER: 60/047,618  
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; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23

28 30 76.9 419 2 US-08-955-471-1  
29 30 76.9 419 4 US-09-667-570A-3  
30 30 76.9 419 5 US-09-667-570A-3  
31 30 76.9 448 4 US-09-457-048B-56  
32 30 76.9 460 2 US-08-756-508-2  
33 30 76.9 460 2 US-08-756-506-4  
34 30 76.9 460 6 5270178-13  
35 30 76.9 460 6 5270178-14  
36 30 76.9 460 6 5270178-15  
37 30 76.9 460 6 5270178-16  
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41 30 76.9 461 6 5270178-18  
42 30 76.9 758 1 US-08-258-188-2  
43 30 76.9 758 1 US-08-526-813-2  
44 30 76.9 758 5 US-09-08554-2  
45 30 76.9 1349 3 US-08-930-291A-6

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3 EARLIER APPLICATION NUMBER: 60/047,507  
4 EARLIER FILING DATE: 1997-05-23  
5 EARLIER APPLICATION NUMBER: 60/047,492  
6 EARLIER FILING DATE: 1997-05-23  
7 EARLIER APPLICATION NUMBER: 60/047,598  
8 EARLIER FILING DATE: 1997-05-23  
9 EARLIER APPLICATION NUMBER: 60/047,613  
10 EARLIER FILING DATE: 1997-05-23  
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12 EARLIER FILING DATE: 1997-05-23  
13 EARLIER APPLICATION NUMBER: 60/047,596  
14 EARLIER FILING DATE: 1997-05-23  
15 EARLIER APPLICATION NUMBER: 60/047,612  
16 EARLIER FILING DATE: 1997-05-23  
17 EARLIER APPLICATION NUMBER: 60/047,632  
18 EARLIER FILING DATE: 1997-05-23  
19 EARLIER APPLICATION NUMBER: 60/047,601  
20 EARLIER FILING DATE: 1997-05-23  
21 EARLIER APPLICATION NUMBER: 60/047,580  
22 EARLIER FILING DATE: 1997-04-11  
23 EARLIER APPLICATION NUMBER: 60/043,568  
24 EARLIER FILING DATE: 1997-04-11  
25 EARLIER APPLICATION NUMBER: 60/043,314  
26 EARLIER FILING DATE: 1997-04-11  
27 EARLIER APPLICATION NUMBER: 60/043,314  
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29 EARLIER APPLICATION NUMBER: 60/043,569  
30 EARLIER FILING DATE: 1997-04-11  
31 EARLIER APPLICATION NUMBER: 60/043,311  
32 EARLIER FILING DATE: 1997-04-11  
33 EARLIER APPLICATION NUMBER: 60/043,671  
34 EARLIER FILING DATE: 1997-04-11  
35 EARLIER APPLICATION NUMBER: 60/043,674  
36 EARLIER FILING DATE: 1997-04-11  
37 EARLIER APPLICATION NUMBER: 60/043,669  
38 EARLIER FILING DATE: 1997-04-11  
39 EARLIER APPLICATION NUMBER: 60/043,312  
40 EARLIER FILING DATE: 1997-04-11  
41 EARLIER APPLICATION NUMBER: 60/043,313  
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43 EARLIER APPLICATION NUMBER: 60/043,672  
44 EARLIER FILING DATE: 1997-04-11  
45 EARLIER APPLICATION NUMBER: 60/043,315  
46 EARLIER FILING DATE: 1997-04-11  
47 EARLIER APPLICATION NUMBER: 60/048,974  
48 EARLIER FILING DATE: 1997-06-06  
49 EARLIER APPLICATION NUMBER: 60/056,886  
50 EARLIER FILING DATE: 1997-08-22  
51 EARLIER APPLICATION NUMBER: 60/056,877  
52 EARLIER FILING DATE: 1997-08-22  
53 EARLIER APPLICATION NUMBER: 60/056,889  
54 EARLIER FILING DATE: 1997-08-22  
55 EARLIER APPLICATION NUMBER: 60/056,893  
56 EARLIER FILING DATE: 1997-08-22  
57 EARLIER APPLICATION NUMBER: 60/056,630  
58 EARLIER FILING DATE: 1997-08-22  
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61 EARLIER APPLICATION NUMBER: 60/056,662  
62 EARLIER FILING DATE: 1997-08-22  
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67 EARLIER APPLICATION NUMBER: 60/056,637  
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74 EARLIER FILING DATE: 1997-08-22  
75 EARLIER APPLICATION NUMBER: 60/056,880  
76 EARLIER FILING DATE: 1997-08-22  
77 EARLIER APPLICATION NUMBER: 60/056,894  
78 EARLIER FILING DATE: 1997-08-22  
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80 EARLIER FILING DATE: 1997-08-22  
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94 EARLIER FILING DATE: 1997-08-22  
95 EARLIER APPLICATION NUMBER: 60/056,894  
96 EARLIER FILING DATE: 1997-08-22  
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98 EARLIER FILING DATE: 1997-08-22  
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100 EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/057,669  
 EARLIER FILING DATE: 1997-09-05  
 EARLIER INVENTOR: JAMES, GUY L.  
 EARLIER FILING DATE: 1997-06-11  
 EARLIER APPLICATION NUMBER: 60/061,060  
 EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 39; DB 4; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Caps 0;  
 Matches 7; Conservative 0; Mismatches 0

QY 1 VPINES 7  
 DB 137 VPINES 143

RESULT 2  
 US-08-169A-1  
 Sequence 1, Application US/07863169A  
 Patent No. 5420245

GENERAL INFORMATION:  
 APPLICANT: BROWN, MICHAEL S.  
 APPLICANT: GOLDSTEIN, JOSEPH L.  
 APPLICANT: REISS, YUVAL  
 TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl  
 TRANSFERASE  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ARNOLD, WHITE & DURKEE  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas

COUNTRY: UNITED STATES OF AMERICA  
 PCT/US/91/02650  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/863,169A  
 FILING DATE: 18-APR-1992  
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/822,011

FILING DATE: 19-JAN-1992

CLASSIFICATION: 530

APPLICATION NUMBER: US 07/937,893

FILING DATE: 18-APR-1991

CLASSIFICATION: 530 US 615,715

APPLICATION NUMBER: 20-NOV-1990

CLASSIFICATION: 530

APPLICATION NUMBER: US 510,706

FILING DATE: 18-APR-1990

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:297/PAR

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 377 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-07-863-169A-1

Query Match 87.2%; Score 34; DB 1; Length 377;

Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Caps 0;

Matches 6; Conservative 0; Mismatches 0

QY 1 VPINES 6

DB 270 VPINES 275

Query Match 87.2%; Score 34; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 3.0; Indels 0; Caps 0;

Matches 6; Conservative 0; Mismatches 0

QY 1 VPINES 6

DB 270 VPINES 275

RESULT 3

US-08-429-964-1

Sequence 1, Application US/08429964

Patent No. 5862243

GENERAL INFORMATION:

APPLICANT: BROWN, MICHAEL S.

APPLICANT: GOLDSTEIN, JOSEPH L.

APPLICANT: REISS, YUVAL

APPLICANT: JAMES, GUY L.

TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL

TRANSFERASE INHIBITORS

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA

PCT/US/91/02650

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429,964

FILING DATE: 18-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,625

FILING DATE: 16-FEB-1993

CLASSIFICATION: 435

APPLICATION NUMBER: US 07/822,011

FILING DATE: 18-APR-1991

CLASSIFICATION: 435

APPLICATION NUMBER: PCT/US/91/02650

FILING DATE: 18-APR-1991

CLASSIFICATION: 435

APPLICATION NUMBER: US 07/615,715

FILING DATE: 20-NOV-1990

CLASSIFICATION: 435 US 07/510,706

APPLICATION NUMBER: 18-APR-1990 (ABANDONED)

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:432/PAR

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2675

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 377 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-429-964-1

Query Match 87.2%; Score 34; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 3.0; Indels 0; Caps 0;

Matches 6; Conservative 0; Mismatches 0

QY 1 VPINES 6

DB 270 VPINES 275

Db 270 VPINES 275

```

RESULT 4
US-07-935-087-1
; Sequence 1, Application US/07935087
; Patent No. 6083917
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: THE IDENTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION,
; TITLE OF INVENTION: AND INHIBITION OF FARNESYL
; TITLE OF INVENTION: PROTEIN TRANSFERASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07935.087
; FILING DATE: 19920824
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US/07/822,011
; FILING DATE: 03/16/92
; NAME: PARKER, DAVID L.
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 32.165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-935-087-1

```

```

Query Match 87.2%; Score 34; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPINES 6
Db 270 VPINES 275

```

```

RESULT 5
PCT-US93-08062-1
; Sequence 1, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: THE IDENTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION,
; TITLE OF INVENTION: AND INHIBITION OF FARNESYL
; TITLE OF INVENTION: PROTEIN TRANSFERASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; ADDRESSEE: THE IDENTIFICATION,
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; OPERATING SYSTEM: IBM PC COMPATIBLE
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08062
; FILING DATE: AUGUST 24, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/935.087
; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32.165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-320-7200
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-08062-1

```

```

Query Match 87.2%; Score 34; DB 5; Length 377;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 VPINES 6
Db 270 VPINES 275

```

```

RESULT 6
US-07-935-169A-5
; Sequence 5, Application US/07863169A
; Patent No. 5420245
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Goldstein, Joseph L.
; APPLICANT: Reiss, Yuval
; TITLE OF INVENTION: Tetrapsptide-Based Inhibitors of Farnesyl
; TITLE OF INVENTION: Transferase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```



TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 INVENTION FOR SEQ ID NO. 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 379 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-429-964-5

Query Match 87.2%; Score 34; DB 2; Length 379;  
 Best Local Similarity 100.0%; Fred. No. 30;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNES 6  
 DB 270 VPHNES 275

RESULT 9  
 US-07-935-087-5

; Sequence 5, Application US/07935087  
 ; Patent No. 6083917  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BROWN, MICHAEL S.  
 ; APPLICANT: ROBERTA M. JOSEPH L.  
 ; APPLICANT: REIS, YUVA  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
 ; TITLE OF INVENTION: THE IDENTIFICATION,  
 ; TITLE OF INVENTION: CHARACTERIZATION,  
 ; TITLE OF INVENTION: AND INHIBITION OF FARNESYL  
 ; TITLE OF INVENTION: PROTEIN TRANSFERASE  
 ; NUMBER OF SEQUENCES: 8  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE  
 ; STREET: P.O. BOX 4433  
 ; CITY: HOUSTON  
 ; STATE: TEXAS  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY DISK/ASKII  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,087  
 ; FILING DATE: 19980824  
 ; PRIORITY APPLICATION DATA:  
 ; PRIOR APPLICATION NUMBER: US/07/822,011  
 ; FILING DATE: 01/16/92  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PARKER, DAVID L.  
 ; REGISTRATION NUMBER: 32,165  
 ; REFERENCE/DOCKET NUMBER: UTSD:269/PAR  
 ; TELEPHONE: 512-320-7200  
 ; TELEFAX: 512-474-7577  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 379 amino acid residues  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-07-935-087-5

Query Match 87.2%; Score 34; DB 3; Length 379;  
 Best Local Similarity 100.0%; Fred. No. 30;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNES 6  
 DB 270 VPHNES 275

RESULT 10  
 PCT-US93-08062-5  
 ; Sequence 5, Application PC/TUS9308062  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; SEQUENCE CHARACTERISTICS:  
 ; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.  
 ; SEQUENCE CHARACTERISTICS: ROBERTA M. JOSEPH L.  
 ; SEQUENCE CHARACTERISTICS: REIS, YUVA  
 ; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.  
 ; ADDRESSEE: METHODS AND COMPOSITIONS FOR  
 ; ADDRESSEE: THE IDENTIFICATION,  
 ; ADDRESSEE: CHARACTERIZATION AND  
 ; ADDRESSEE: INHIBITION OF  
 ; ADDRESSEE: FARNESYLTRANSFERASE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE  
 ; STREET: P.O. BOX 4433  
 ; CITY: HOUSTON  
 ; STATE: TEXAS  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY DISK/ASKII  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WORDPERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/08062  
 ; FILING DATE: 24 AUGUST 1992  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION NUMBER: 07/935,087  
 ; FILING DATE: 24 AUGUST 1992 (24.08.92)  
 ; NAME: UNKNOWN  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PARKER, DAVID L.  
 ; REGISTRATION NUMBER: 32,165  
 ; REFERENCE/DOCKET NUMBER: UTSD:269/PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 512-320-7200  
 ; TELEFAX: 512-474-7577  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 379 amino acid residues  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; PCT-US93-08062-5

Query Match 87.2%; Score 34; DB 5; Length 379;  
 Best Local Similarity 100.0%; Fred. No. 30;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPHNES 6  
 DB 270 VPHNES 275

RESULT 11  
 PCT-US93-10442-8  
 ; Sequence 8, Application PC/TUS9310442  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Omer, Charles A  
 ; APPLICANT: Diehl, Ronald E  
 ; APPLICANT: Gibbs, Jackson B

```

; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferrase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10442
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/968,782
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; PCT-US93-10442-8

```

```

Query Match      87.2% Score 34; DB 5; Length 379;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 1 VPINES 6
DB 270 VPINES 275

```

```

RESULT 12
; US-08-424-268-20
; Sequence 20, Application US/08424268
; Patent No. 5821118
; GENERAL INFORMATION:
; APPLICANT: Omet, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferrase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Mac
; OPERATING SYSTEM: System 7.5.3
; SOFTWARE: Microsoft Word 5.1

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,268
; FILING DATE: 4/24/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; US-08-424-268-20

```

```

Query Match      87.2% Score 34; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 1 VPINES 6
DB 710 VPINES 715

```

```

RESULT 13
; PCT-US93-10442-20
; Sequence 20, Application PC/TUS9310442
; GENERAL INFORMATION:
; APPLICANT: Omet, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferrase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10442
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/968,782
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: N-terminal  
 PCT-U0593-10442-20

Query Match 87.2%, Score 34, DB 5, Length 819;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 VPNESE 6  
 DB 710 VPNESE 715

RESULT 14  
 US-08-173-5108-88  
 ; Sequence 88, Application US/081735108  
 ; Patent No. 5747296  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATTHEW MOYLE, ET AL.  
 ; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
 ; NUMBER OF SEQUENCES: 104  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/173,5108  
 ; FILING DATE: 23-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/151,064  
 ; FILING DATE: 10-NOV-1993  
 ; APPLICATION NUMBER: 08/060,433  
 ; FILING DATE: 11-MAY-1993  
 ; APPLICATION NUMBER: 07/996,972  
 ; FILING DATE: 24-DEC-1992  
 ; APPLICATION NUMBER: 07/881,721  
 ; FILING DATE: 11-MAY-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BIGGS, SUZANNE L.  
 ; REGISTRATION NUMBER: 30,158  
 ; REFERENCE/DOCKET NUMBER: 203/226  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 88:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 146 AMINO ACIDS  
 ; TYPE: AMINO ACIDS  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: PEPTIDE

US-08-173-5108-88

Query Match 79.5%, Score 31, DB 1, Length 146;  
 Best Local Similarity 83.3%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 2 PHNESE 7  
 DB 25 PHNEGE 30

## RESULT 15

US-08-458-218-86  
 ; Sequence 86, Application US/08458218  
 ; Patent No. 5789178  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATTHEW MOYLE ET AL.  
 ; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
 ; NUMBER OF SEQUENCES: 102  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,218  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/151,064  
 ; FILING DATE: 10-NOV-1993  
 ; APPLICATION NUMBER: 08/060,433  
 ; FILING DATE: 11-MAY-1993  
 ; APPLICATION NUMBER: 07/881,721  
 ; FILING DATE: 11-MAY-1992  
 ; APPLICATION NUMBER: 07/996,972  
 ; FILING DATE: 24-DEC-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BIGGS, SUZANNE L.  
 ; REGISTRATION NUMBER: 30,158  
 ; REFERENCE/DOCKET NUMBER: 203/226  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 86:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 145 AMINO ACIDS  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: PEPTIDE

US-08-458-218-86

Query Match 79.5%, Score 31, DB 1, Length 146;  
 Best Local Similarity 83.3%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 2 PHNESE 7  
 DB 25 PHNEGE 30

Search completed: May 6, 2003, 15:04:07  
 Job time : 12.2 secm



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# OM protein - protein search, using sw model

Run on: May 6, 2003, 14:57:44 ; Search time 31.85 seconds  
(without alignments)  
29.286 Million cell updates/sec

Title: US-09-851-422b-8

Perfect score: 31

Sequence: 1 VPNESE 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 03

Maximum March 03

Listing first 45 summaries

## Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	36	92.3	242	21 AAG09225	Arabisopsis thalia
3	36	92.3	242	21 AAG09225	Arabisopsis thalia
4	36	92.3	315	21 AAG09223	Arabisopsis thalia
5	34	87.2	13	12 AAR14717	Farnesyl-protein t
6	34	87.2	293	21 AAG30075	Arabisopsis thalia
7	34	87.2	377	15 AAR49739	Farnesyltransferas
8	34	87.2	377	16 AAR77839	Rat farnesyl prote
9	34	87.2	17	AAW04427	Mouse ischaemic co
10	34	87.2	377	23 ABB57154	

11	34	87.2	379	15 AAR49734	Farnesyltransferas
12	34	87.2	379	15 AAR54830	Alpha subunit of h
13	34	87.2	379	16 AAR77841	Human farnesyl pro
14	34	87.2	379	17 AAR77841	Human farnesyl pro
15	34	87.2	379	21 ABB08436	Protein sequence 2
16	34	87.2	380	21 AAR77150	Human geranylgeran
17	34	87.2	384	21 AAB58384	Lung cancer associ
18	32	82.1	155	22 ABB68133	Drosophila melanog
19	32	82.1	198	22 ABB68133	Novel human diagno
20	32	82.1	332	21 AAG55461	Arabisopsis thalia
21	32	82.1	332	21 AAG55461	Arabisopsis thalia
22	32	82.1	1639	23 ABB59281	Drosophila melanog
23	31	79.5	71	23 ABB03959	Human ORFX protein
24	31	79.5	87	18 AAW56567	H. pylori ORF 11ae
25	31	79.5	100	18 AAW56567	H. pylori ORF 11ae
26	31	79.5	146	14 AAR52989	Canine hookworm ne
27	31	79.5	146	20 AAY23597	Canine hookworm ne
28	31	79.5	59	22 ABB62607	Drosophila melanog
29	31	79.5	59	22 ABB62607	Drosophila melanog
30	30	76.9	78	12 AAR5744	R18 antigen of HTL
31	30	76.9	23	23 ABB83175	Streptococcus suis
32	30	76.9	235	22 ABB02914	Novel human diagno
33	30	76.9	258	12 AAR13048	Protein C heavy ch
34	30	76.9	261	14 AAR30723	Protein C heavy ch
35	30	76.9	262	12 AAR13047	Protein C heavy ch
36	30	76.9	262	12 AAR13724	Protein C heavy ch
37	30	76.9	262	12 AAR13724	Protein C heavy ch
38	30	76.9	262	12 AAR12192	Human protein C ca
39	30	76.9	262	12 AAR12193	Human protein C ca
40	30	76.9	262	12 AAR12194	Human protein C ca
41	30	76.9	262	12 AAR12195	Human protein C ca
42	30	76.9	262	12 AAR12196	Human protein C ca
43	30	76.9	263	15 AAG26554	Activated modified
44	30	76.9	272	21 AAG21570	Arabisopsis thalia
45	30	76.9	323	21 AAG21569	Arabisopsis thalia

## ALIGNMENTS

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DT 18-DEC-2001 (first entry)  
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DE Human, vaccination; gene therapy; nutritional supplement;  
X stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
X immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
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XX 25-OCT-2001.  
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XX Tang YT, Liu C, Dumanan RT;  
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XX Nucleic acids encoding a range of human polypeptides, useful in genetic  
X vaccination, testing and therapy -  
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2

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XX Arabidopsis thaliana protein fragment SEQ ID NO: 35991.  
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 KW hybridization assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
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 CS Arabidopsis thaliana.  
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 DB 74 VPINES 79

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 ID AAR49739 standard; Protein; 377 AA.  
 AC AAR49739;  
 XX 08-AUG-1994 (first entry)  
 XX AAR49739;  
 DE Farnesyltransferase alpha-subunit.  
 XX Farnesyltransferase; FT; alpha-subunit; p21ras; ras protein;  
 KW cancer therapy.  
 XX Rattus sp.  
 OS

-XX MO9404561-A.  
 XX 03-MAR-1994.  
 XX 24-AUG-1993; 93MO-US08062.  
 XX 24-AUG-1992; 92US-0935087.  
 XX (GETH ) GENENTECH INC.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Brown MS, Goldstein JL, Marsters JC, Reiss Y;  
 WPI; 1994-083105/10.  
 DR N-PSDB; AAQ44397.  
 XX New farnesyl-transferase inhibitors - used for inhibiting  
 PT attachment of a farnesyl moiety to a p21ras protein in malignant  
 PT cells  
 PS Disclosure; Page 116-118; 183pp; English.  
 CC The cDNA (AAQ44397) and amino acid (AAR49739) sequences of rat  
 CC farnesyltransferase (FT) alpha-subunit were determined. The cDNA  
 CC can be used to produce recombinant FT, useful for screening  
 CC potential anticancer agents that prevent expression of p21ras.  
 XX Sequence 377 AA;  
 Query Match 87.2%; Score 34; DB 15; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 OY 1 VPINES 6  
 DB 270 VPINES 275

RESULT 8  
 ID AAR77839  
 ID AAR77839 standard; Protein; 377 AA.  
 AC AAR77839;  
 XX 23-JAN-1996 (first entry)  
 DT Rat farnesyl protein transferase alpha subunit.  
 XX Farnesyl transferase; inhibitor; cancer; ras; p21.

XX Rattus sp.  
 XX US5420345-A.  
 XX 30-MAY-1995.  
 XX 18-APR-1990; 90US-0510706.  
 XX 16-JAN-1992; 92US-0822011.  
 XX 18-APR-1990; 90US-0510706.  
 XX 20-NOV-1990; 90US-0615715.  
 XX 03-APR-1992; 92US-0863169.  
 XX (TEXA ) UNIV TEXAS.  
 XX Brown MS, Goldstein JL, Reiss Y;  
 WPI; 1995-206308/27.  
 DR N-PSDB; AAQ94410.  
 XX New farnesyl transferase inhibitor peptide(s) - based on farnesyl  
 PT acceptor substrate carboxy terminal sequences, used for the



PT treatment of cancer  
 PS Example 3; Column 47-50; 55pp; English.  
 XX  
 CC AAR7839 is the alpha subunit of rat farnesyl transferase which  
 CC is involved in the farnesylation of various cellular proteins  
 CC including the cancer related ras proteins. It is used to produce the  
 CC complete farnesyl transferase molecule which is used to demonstrate  
 CC the effectiveness of peptide inhibitors capable of inhibiting  
 CC farnesyl transferases. The peptide inhibitors are useful for  
 CC treating cancers and ras-related cancers in particular.  
 XX  
 SQ Sequence 377 AA;  
 Query Match 87.2%; Score 34; DB 16; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPINES 6  
 DB 270 VPINES 275  
 |||||  
 RESULT 9  
 AAM04427 standard; Protein; 377 AA.  
 ID AAM04427  
 AC AAM04427;  
 XX  
 DT 30-JUL-1997 (first entry)  
 XX  
 DE Rat farnesyl transferase enzyme alpha subunit.  
 XX  
 KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;  
 XX ras protein; K-ras B; malignant; detection; identification.  
 XX  
 OS Rattus rattus.  
 XX  
 PN MO9634113-A2.  
 XX  
 XX 31-OCT-1996.  
 XX  
 PF 29-APR-1996; 96MO-US05969.  
 XX  
 PR 27-APR-1995; 95US-0429964.  
 XX  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 XX  
 XX Brown MS, Goldstein JL, James GL;  
 XX WPI; 1956-497642/49.  
 XX N-PSDB; AAT38708.  
 XX  
 XX Assay for farnesyl transferase activity - by determining ability to  
 XX transfer farnesyl moiety to K-ras B protein, partic. useful for  
 XX identifying inhibitors  
 XX  
 PS Example 3; Page 137-140; 257pp; English.  
 XX  
 CC AAM04427 shows the alpha subunit of a farnesyl transferase (FT) enzyme  
 CC derived from rat brain tissue. The enzyme was used in a method  
 CC for identifying FT inhibitors. The method involved screening candidate  
 CC compounds for the ability to inhibit the transfer of a farnesyl moiety  
 CC to a K-ras B protein. FT inhibitors act by blocking the attachment of  
 CC farnesyl moieties to the protein. Proteins in malignant cells of patients suffering  
 CC from cancer or precancerous states, and as such are used to treat such  
 CC conditions.  
 XX  
 SQ Sequence 377 AA;  
 Query Match 87.2%; Score 34; DB 17; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPINES 6  
 DB 270 VPINES 275  
 |||||

QY 1 VPINES 6  
 DB 270 VPINES 275  
 |||||  
 RESULT 10  
 ABB57154  
 ID ABB57154 standard; Protein; 377 AA.  
 XX  
 XX ABB57154;  
 XX  
 DT 07-MAR-2002 (first entry)  
 XX  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:375.  
 XX  
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 XX vasoaplastic ischaemia; ischaemic condition; ischaemic disease.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200188188-A2.  
 XX  
 XX 22-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001MO-JP04192.  
 XX  
 PR 18-MAY-2000; 2000JP-0145977.  
 XX  
 PA (UTNT-) UNIV NIHOH SCHOOL JURIDICAL PERSON.  
 XX  
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 XX WPI; 2002-034733/04.  
 XX N-PSDB; ABI99411.  
 XX  
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 XX expression levels of particular genes defined in the specification or  
 XX by determining the expression profile of a gene group comprising these  
 XX genes -  
 XX  
 CC Claim 2; Page 1003-1004; 2690pp; English.  
 XX  
 CC The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasoaplastic ischaemia) by measuring  
 CC expression levels of particular genes (ABI99202 to ABI99912), encoding  
 CC the genes (I), in a test sample or determining the expression profile  
 CC of expression levels of a gene group comprising these genes. The  
 CC expression levels or expression profiles produced by these genes are  
 CC used as an indicator when screening for ischaemic condition-improving  
 CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
 CC represent PCR primers for a mouse ischaemic condition related sequence,  
 CC which are used in the exemplification of the present invention.  
 XX  
 XX Sequence 377 AA;  
 XX  
 SQ  
 Query Match 87.2%; Score 34; DB 23; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPINES 6  
 DB 270 VPINES 275  
 |||||  
 RESULT 11  
 AAR49734  
 ID AAR49734 standard; Protein; 379 AA.  
 XX

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AC AAR49734;
AD
DT 08-AUG-1994 (first entry)
DX
XX Farnesyltransferase alpha-subunit.
XX
KW Farnesyltransferase; FT; alpha-subunit; p21ras; ras protein;
KW cancer therapy.
XX
XX Homo sapiens.
XX
XX MO9404561-A.
XX
PD 03-MAR-1994.
XX
XX 24-AUG-1993; 93MO-US08062.
XX
PR 24-AUG-1992; 92US-0935087.
XX
XX (GENTH ) GENENTECH INC.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, Marsters JC, Reiss Y;
DR
DR N-PSDB; AAR44395.
XX
XX New farnesyl-transferase inhibitors - used for inhibiting
XX attachment of a farnesyl moiety to a p21ras protein in malignant
XX cells
XX
PS Disclosure; Fig 26; 183pp; English.
XX
CC The cDNA (AAQ44395) and amino acid (AAR49734) sequences of human
CC farnesyltransferase (FT) alpha-subunit were determined. The cDNA
CC was used to produce recombinant FT, useful for screening
CC potential anticancer agents that prevent expression of p21ras.
XX
SQ Sequence 379 AA;

Query Match 87.2%; Score 34; DB 15; Length 379;
Best Local Similarity 100.0%; Pred. NO. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPINES 6
DB 270 VPINES 275

RESULT 12
IN AAR54830 standard; Protein; 379 AA.
AC AAR54830;
AD
DT 07-NOV-1994 (first entry)
DX
XX Alpha subunit of human FRTase.
XX
KW Farnesyl protein transferase; inhibition; farnesylation.
XX
XX Homo sapiens.
XX
XX MO9410184-A.
XX
XX 11-MAY-1994.
XX
XX 29-OCT-1993; 93MO-US10442.
XX
PR 30-OCT-1992; 92US-0968782.
XX
XX (MERI ) MERCK & CO INC.
XX
XX

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PI Diehl RE, Gibbs JB, Kohl NE, Omer CA;
XX
DR WPI; 1994-167373/20.
DR N-PSDB; AAQ44887.
XX
XX Mammalian farnesyl protein transferase prodn. - used in assays
XX for farnesyl transferase activity for the identification of
XX anticancer agents
XX
XX Disclosure; Fig 2; 69pp; English.
XX
CC The cDNA encoding the human alpha subunit of FRTase was isolated
CC from a human placental cDNA library in lambda gtl1 using a bovine
CC FRTase cDNA probe. The FRTase can be used to assess the inhibitory
CC activity of various compounds in the presence of a suitable substrate.
CC The assay can be used to identify anticancer agents.
XX
XX See also AAR54829-32.
XX
SQ Sequence 379 AA;

Query Match 87.2%; Score 34; DB 15; Length 379;
Best Local Similarity 100.0%; Pred. NO. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPINES 6
DB 270 VPINES 275

RESULT 13
IN AAR77841 standard; Protein; 379 AA.
ID AAR77841
XX
AC AAR77841;
XX
DT 23-JAN-1996 (first entry)
DX
XX Human farnesyl protein transferase alpha subunit.
XX
KW Farnesyl transferase; inhibitor; cancer; ras; p21.
XX
OS Homo sapiens.
XX
XX US5420245-A.
XX
PD 30-MAY-1995.
XX
XX 18-APR-1990; 90US-0510706.
XX
XX 16-JAN-1992; 92US-0822011.
XX 18-APR-1990; 90US-0510706.
XX 03-APR-1990; 90US-0637519.
XX 03-APR-1992; 92US-0863169.
XX (TEXA ) UNIV TEXAS.
XX
XX Brown MS, Goldstein JL, Reiss Y;
XX
XX WPI; 1995-206308/27.
XX N-PSDB; AAQ94412.
XX
XX New farnesyl transferase inhibitor peptide(a) - based on farnesyl
XX acceptor substrate carboxy terminal sequences, used for the
XX treatment of cancer
XX
XX Example 4; Column 55-58; 55pp; English.
XX
XX AAR77841 is the alpha subunit of human farnesyl transferase which
XX is involved in the farnesylation of various cellular proteins
XX including the cancer related ras proteins. It is used to produce the
XX complete farnesyl transferase molecule which is used to demonstrate
XX the effectiveness of peptide inhibitors capable of inhibiting
XX farnesyl transferases. The peptide inhibitors are useful for

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CC treating cancers and ras-related cancers in particular.
XX
SQ
Sequence 379 AA;
Query Match 87.2%; Score 34; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VPHNES 6
| | | | |
DB 270 VPHNES 275

RESULT 14
AAW04431
ID AAW04431 standard; Protein; 379 AA.
AC
AC AAW04431;
XX
XX
DT 30-JUL-1997 (first entry)
XX
XX Human farnesyl transferase enzyme subunit.
DE
XX Farnesyl transferase; inhibitor; capcer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification.
XX
OS Homo sapiens.
XX
XX WO9634113-A2.
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96WO-US05969.
XX
XX 27-APR-1995; 95US-0429964.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Brown MS, Goldstein JL, James GL;
PI
XX WPI; 1996-497642/49.
DR
XX N-PSDB; AAT36710.
XX
XX Assay for farnesyl transferase activity - by determining ability to
PT transfer farnesyl moiety to K-ras B protein, partic. useful for
PT identifying inhibitors
XX
XX Example 4; Page 151-154; 257pp; English.
XX
XX AAW04431 shows the alpha subunit of a farnesyl transferase (FT) enzyme
CC derived from a human retinal cDNA library. The enzyme was used in a
CC method for identifying FT inhibitors. The method involved screening
CC candidate compounds for the ability to inhibit the transfer of a
CC farnesyl moiety to K-ras B protein. FT inhibitors act by blocking
CC the attachment of prenyl groups to ras proteins in malignant cells of
CC patients suffering from cancer or precancerous states, and as such are
CC used to treat such conditions.
XX
SQ Sequence 379 AA;
Query Match 87.2%; Score 34; DB 17; Length 379;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VPHNES 6
| | | | |
DB 270 VPHNES 275

RESULT 15
ABW08436
ID ABW08436 standard; Protein; 379 AA.
XX

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AC ABW08436;
XX
XX 07-MAY-2002 (first entry)
XX
DE Protein sequence 2 relative to the farnesyltransferase of the invention.
XX
XX Farnesyltransferase; enzyme.
XX
XX Unidentified.
XX
XX X898075770-A.
XX
XX 16-NOV-1998.
PD
XX 01-APR-1997; 97KR-0012067.
PF
XX 01-APR-1997; 97KR-0012067.
PR
XX (GLDS ) LG CHEM LTD.
XX
XX Moon GD, Kim MJ, Chung HH;
PI
XX WPI; 2000-020309/02.
DR
XX N-PSDB; ABA98898.
XX
XX Farnesyltransferase having histidine tag and process for preparing the
PT same.
XX
XX Disclosure; Page 16-17; 23pp; Korean.
XX
XX The invention relates to a farnesyltransferase with a histidine tag,
CC and methods for preparing it. The current sequence represents protein
CC sequence 2 relative to the farnesyltransferase of the invention.
XX
XX Sequence 379 AA;
SQ
Query Match 87.2%; Score 34; DB 21; Length 379;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VPHNES 6
| | | | |
DB 270 VPHNES 275
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